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(STIC)

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Access DB# 71349

SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name: Dan Lin Examiner #: 69507 Date: 7-18-02
 Art Unit: 1646 Phone Number 30 8-4008 Serial Number: 09/698419
 Mail Box and Bldg/Room Location: CMI 6B02 Results Format Preferred (circle): PAPER DISK E-MAIL

If more than one search is submitted, please prioritize searches in order of need.

 Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: _____

Inventors (please provide full names): _____

Earliest Priority Filing Date: _____

For Sequence Searches Only Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.

please search SEQ ID NO: 14
 of 09/698419.

Edward Hart
 Technical Info. Specialist
 STIC/Biotech
 CMI 6B02 Tel: 305-9203

10 COI

STAFF USE ONLY

Searcher: _____

Searcher Phone #: _____

Searcher Location: _____

Type of Search

NA Sequence (#) _____

AA Sequence (#) _____

Structure (#) _____

Riblinoranthic

Vendors and cost where applicable

STN _____

Dialog _____

Questel/Orbit _____

Dr.Link _____

prot. 14

7/19/02

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 19, 2002, 14:36:59 ; Search time 13.07 Seconds

(without alignments)
691,467 Million cell updates/sec

Title: US-09-698-419-14

Perfect score: 1963
Sequence: 1 MAMSHADNITLQNLSPFLA.....STLLYCKRSLRPPPCVY 370

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: /cgn2_6/ptodata/2/1aa/5A.COMB.pep:*
2: /cgn2_6/ptodata/2/1aa/5B.COMB.pep:*
3: /cgn2_6/ptodata/2/1aa/6A.COMB.pep:*
4: /cgn2_6/ptodata/2/1aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/2/1aa/PCRTUS.COMB.pep:*
6: /cgn2_6/ptodata/2/1aa/Backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1963	100.0	370	3	US-09-251-373-2
2	264.5	13.5	478	3	US-09-292-071-31
3	264.5	13.5	478	4	US-09-292-069A-31
4	258	13.1	470	4	US-09-292-071-25
5	258	13.1	470	4	US-09-292-069A-25
6	257.5	13.1	453	1	US-08-570-157-7
7	256.5	13.1	478	3	US-09-292-071-33
8	256.5	13.1	478	4	US-09-292-069A-33
9	255	13.0	330	1	US-08-118-270-19
10	255	13.0	330	5	PCR-US93-08528-19
11	253.5	12.9	471	1	US-08-370-542-7
12	253.5	12.9	471	1	US-07-817-920-8
13	253.5	12.9	471	1	US-08-117-006-8
14	253.5	12.9	471	1	US-08-216-594-8
15	253.5	12.9	471	1	US-08-542-358-7
16	253.5	12.9	471	2	US-08-244-434-2
17	253.5	12.9	471	2	US-09-018-351-7
18	253.5	12.9	471	4	US-09-032-742-8
19	253.5	12.9	471	5	PCR-US93-00149-8
20	253	12.9	448	1	US-08-570-157-3
21	251	12.8	471	4	US-09-032-742-11
22	251	12.8	471	4	US-07-996-772A-11
23	250	12.7	471	4	US-09-032-742-11
24	250	12.7	471	4	US-09-032-742-2
25	250	12.7	471	4	US-09-032-742-14
26	248.5	12.7	357	1	US-08-356-405-2
27	247.5	12.6	447	1	US-07-937-609-29

28	247.5	12.6	447	1	US-07-978-892A-6	Sequence 6, Appl1
29	247.5	12.6	447	4	US-08-029-170-29	Sequence 29, Appl1
30	243.5	12.4	388	1	US-08-446-822-8	Sequence 8, Appl1
31	243.5	12.4	388	5	PCT-US93-12586-8	Sequence 10, Appl1
32	243	12.4	353	2	US-08-467-559B-10	Sequence 16, Appl1
33	243	12.4	452	1	US-07-937-609-16	Sequence 16, Appl1
34	243	12.4	452	4	US-08-029-170-16	Sequence 16, Appl1
35	242.5	12.4	357	2	US-08-031-538-4	Sequence 4, Appl1
36	241.5	12.3	460	1	US-07-817-920-4	Sequence 4, Appl1
37	241.5	12.3	460	1	US-07-996-772A-9	Sequence 9, Appl1
38	241.5	12.3	460	1	US-08-370-542-4	Sequence 4, Appl1
39	241.5	12.3	460	1	US-08-117-006-4	Sequence 4, Appl1
40	241.5	12.3	460	1	US-08-216-594-4	Sequence 4, Appl1
41	241.5	12.3	460	1	US-08-342-358-4	Sequence 4, Appl1
42	241.5	12.3	460	3	US-09-018-351-4	Sequence 4, Appl1
43	241.5	12.3	460	4	US-09-032-742-4	Sequence 4, Appl1
44	241.5	12.3	460	5	PCT-US93-00149-4	Sequence 4, Appl1
45	241	12.3	458	1	US-08-310-271-2	Sequence 2, Appl1

ALIGNMENTS

RESULT 1
Sequence 2 Application US/09251373
Patent No. 6071722
GENERAL INFORMATION:
APPLICANT: SHABON, USMAN
APPLICANT: ELSHOUBACH, NABIL
TITLE OF INVENTION: A G-PROTEIN COUPLED 7TM RECEPTOR
TITLE OF INVENTION: (AXOR-1)
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ratner & Prestia
STREET: P.O. Box 980
CITY: Valley Forge
STATE: PA
COUNTRY: USA
ZIP: 19482

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Fastseq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/251,373
FILING DATE: 16-FEB-1999
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 60/082,981
FILING DATE: 24-APR-1998
APPLICATION NUMBER: 60/089,639
FILING DATE: 17-JUN-1998
ATTORNEY/AGENT INFORMATION:
NAME: Prestia, Paul F.
REGISTRATION NUMBER: 23,031
REFERENCE/DOCKET NUMBER: GP-70432
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-407-0700
TELEFAX: 610-407-0700
TELEX: 846169

SEQUENCE CHARACTERISTICS:
LENGTH: 370 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-251-373-2

Query Match 100.0%; Score 1963; DB 3; Length 370;
 Best Local Similarity 100.0%; Pred. No. 4,4e-169;
 Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MANYSHADNIIQNTSPLTAFLKLSLGLIGSVGNLLISLLVKDKTLHAPYFLL 60
 DB 1 MANYSHADNIIQNTSPLTAFLKLSLGLIGSVGNLLISLLVKDKTLHAPYFLL 60
 QY 61 DLCCSDILRSACFPFVFNKSGSTWYGTLLCKVIAELGLVSCPHTAFLMFCISVTRY 120
 DB 61 DLCCSDILRSACFPFVFNKSGSTWYGTLLCKVIAELGLVSCPHTAFLMFCISVTRY 120
 QY 121 LAIAHRRYTKLTFWTCLAVICMWTLSVAAAPPVLDVGTSYFIREDOCTFOHRSR 180
 DB 121 LAIAHRRYTKLTFWTCLAVICMWTLSVAAAPPVLDVGTSYFIREDOCTFOHRSR 180
 QY 181 ANDSGFMILLALITATOLVYLKLFYHDKRKKMPVOFVAASQNTFPHGASGQA 240
 DB 181 ANDSGFMILLALITATOLVYLKLFYHDKRKKMPVOFVAASQNTFPHGASGQA 240
 QY 241 ANMLAGFGRPPTLLGIRONANTGRRLLVLDEFKMEKRISRMFYIMTFELTLMGP 300
 DB 241 ANMLAGFGRPPTLLGIRONANTGRRLLVLDEFKMEKRISRMFYIMTFELTLMGP 300
 QY 301 YLVACYWRFAGPVPGFELTAAYMASFAQAGINPVCIFSNRELRCESTLLTCRKS 360
 DB 301 YLVACYWRFAGPVPGFELTAAYMASFAQAGINPVCIFSNRELRCESTLLTCRKS 360
 QY 361 RLREPCYVI 370
 DB 361 RLREPCYVI 370

RESULT 2

US-09-292-071-31
 ; Sequence 31, Application US/09292071
 ; Patent No. 6107324
 ; GENERAL INFORMATION:
 ; APPLICANT: Behan, Dominic
 ; APPLICANT: Chalmers, Derek
 ; TITLE OF INVENTION: No. 6107324-Endogenous, Constitutively Activated
 ; TITLE OF INVENTION: Human Serotonin Receptors and Small Molecule Modulators Thereof
 ; NUMBER OF SEQUENCES: 33
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Arena Pharmaceuticals, Inc.
 ; STREET: 6166 Nancy Ridge Drive
 ; CITY: San Diego
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 92121
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/292,071
 ; FILING DATE: April 14, 1999
 ; CLASSIFICATION:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Mark J. Rosen
 ; REGISTRATION NUMBER: 39,822
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (215) 564-6525
 ; TELEFAX: (215) 568-3439
 ; INFORMATION FOR SEQ ID NO: 31:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 478 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS:
 ; TOPOLOGY: not relevant
 ; MOLECULE TYPE: protein
 ; US-09-292-071-31

Query Match 13.5%; Score 264.5; DB 3; Length 478;
 Best Local Similarity 23.9%; Pred. No. 3.6e-16;
 Matches 83; Conservative 61; Mismatches 153; Indels 51; Gaps 9;

QY 30 IIVSVGNLLISLLVKDKTLHAPYFLLDLCCSDILRSACFPFVFNKSGSTWY 89
 DB 84 VILITAGNLVIMASLEKRLONATNYFLMSLAIDMLGFLVPMVSMILLYGYMPL 143
 QY 90 GTLLCKVIAELGLVSCPHTAFLMFCISVTRYLAIA---HHREYTKLTFWTCLAVICM 145
 DB 144 PSKLCANWYLDVLFSTASIMHLCAISLDRYVAQNIIHRSFRSKAFKIIA---V 199
 QY 146 WTLVSAAPF-PVLDVGTSYFIREDOCTFOHNSFRANDSLGFMILLALITATOLVYLK 204
 DB 200 WTLVSGISMPILPFGLODDSKVEKESCLLADDFVLIGSFVSFFILITWITYFLTIK 259
 QY 205 L-----IFFYHDKRKKMP---VOFVAASQNTFPHGASGQAANMLAGFGRPPTL 256
 DB 260 VLRRQALMLHGTETPEPPGLSLDFLKCKCRN-----TAEBENSAN----- 299
 QY 257 LGIRONANTGRRRL-----VLDEFKMEKRISRMFYIMTFELTLMGPVACYWRY 309
 DB 300 ----PNDQARRKKRRERPRGTMQAINNERKSKVLGIVFLFYVMWMCFFITINAV 355
 QY 310 FAR---GPVPGFELTAAYMASFAQAGINPVCIFSNRELRCESTLL 354
 DB 356 ICKESCNEVDIYALLNVFWIGLYLSAVNPLVYTLFNKITYRARSNTL 403

RESULT 3

US-09-292-069A-31
 ; Sequence 31, Application US/09292069A
 ; Patent No. 6140509
 ; GENERAL INFORMATION:
 ; APPLICANT: Behan, Dominic P
 ; APPLICANT: Chalmers, Derek T
 ; APPLICANT: Foster, Richard J
 ; APPLICANT: Glen, Robert C
 ; APPLICANT: Lawless, Michael S
 ; APPLICANT: Liaw, Chen W
 ; APPLICANT: Liu, Qian
 ; APPLICANT: Russo, Joseph F
 ; APPLICANT: Smith, Julian R
 ; APPLICANT: Thomsen, William J
 ; TITLE OF INVENTION: No. 6140509-Endogenous, Constitutively Activated Human
 ; TITLE OF INVENTION: Serotonin Receptors and Small Molecule Modulators
 ; TITLE OF INVENTION: Thereof
 ; FILE REFERENCE: AREN0033
 ; CURRENT APPLICATION NUMBER: US/09/292,069A
 ; CURRENT FILING DATE: 1999-04-14
 ; PRIOR APPLICATION NUMBER: 60/090,783
 ; PRIOR FILING DATE: 1998-06-26
 ; PRIOR APPLICATION NUMBER: 60/112,909
 ; PRIOR FILING DATE: 1998-12-18
 ; PRIOR APPLICATION NUMBER: 60/123,000
 ; PRIOR FILING DATE: 1999-03-05
 ; NUMBER OF SEQ ID NOS: 33
 ; SOFTWARE: Patentin Ver. 2.1
 ; SEQ ID NO 31
 ; LENGTH: 478
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: No. 6140509e1
 ; OTHER INFORMATION: Sequence
 ; US-09-292-069A-31

Query Match 13.5%; Score 264.5; DB 4; Length 478;
 Best Local Similarity 23.9%; Pred. No. 3.6e-16;
 Matches 83; Conservative 61; Mismatches 153; Indels 51; Gaps 9;

QY 30 IIGSVVGNLLISILYKDKTLHRAVYFLLDCCSDLSAICFPFVNSVKNSTWY 89
 DB 84 VILLTAGNLTMAVSLKELONATYFLMSLAIDMLGFLVMPVSMITLYGRMPL 143
 QY 90 GELTKVIAFLVGLSCFHFAMFECISVTRYLAIA-----HHREYTKRLTEWTCIAICMV 145
 DB 144 PSLKCAVWIYLDVLFSTASIMHLCALISLDKRYAQNPIHHSRFSKRAFLKITA-----V 199
 QY 146 WFLSVMAFP-PVLDVGYTSFIREDOCTQHRSFRANDSLGFMILLALILATOLVYLK 204
 DB 200 WRTISVGISMPVPEGLDDSKVKEGSCLLADNDFVLIGSVSPFIPLTIMVITYFLIK 259
 QY 205 L-----IFVHDKRKKP---VOPVAASQNMTHFGGASQAANLACGRCPTPEPL 256
 DB 260 VLRQALMLHGTPEPPGISLDFLCKCKRN-----TAEENSAN----- 299
 QY 257 LGIRONANTGRRRL-----VLDEFKMEKRISRMFYMTFLFLMGPIVACVYRV 309
 DB 300 ---PQODONARRKKRRPRCTMOAINNERKASKVLGIVFLELVMMCPFITINMAV 355
 QY 310 FAR---GPVPPGFLTAAVWMSFAQGINPFVCIFSNRELRCPSTL 354
 DB 356 ICKESCNEVIGALLNVFWIGILSSAVNPLYTLFKITRRASNTL 403

RESULT 4
 US-09-292-071-25
 ; Sequence 25, Application US/09292071
 ; Patent No. 6107324

GENERAL INFORMATION:
 APPLICANT: Behan, Dominic
 APPLICANT: Chalmers, Derek
 TITLE OF INVENTION: No. 6107324-Endogenous, Constitutively Activated
 TITLE OF INVENTION: Human Serotonin Receptors and Small Molecule Modulators Thereof
 NUMBER OF SEQUENCES: 33
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Arena Pharmaceuticals, Inc.
 STREET: 6166 Nancy Ridge Drive
 CITY: San Diego
 STATE: CA
 COUNTRY: USA
 ZIP: 92121

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/292,071
 FILING DATE: April 14, 1999
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Mark J. Rosen
 REGISTRATION NUMBER: 39,822
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (215) 564-6525
 TELEFAX: (215) 568-3439
 INFORMATION FOR SEQ ID NO: 25:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 470 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: not relevant
 MOLECULE TYPE: protein
 US-09-292-071-25

Query Match 13.1%; Score 258; DB 3; Length 470;
 Best Local Similarity 24.7%; Pred. No. 1,4e-15;
 Matches 89; Conservative 63; Mismatches 155; Indels 54; Gaps 12;

QY 15 LSPITAFKLTSLGF-----IIGSVVGNLLISILYKDKTLHRAVYFLLDCCSDI 67

DB 61 LSPSCSLHLDQEKNSALLTAVIITLTAGNLTMAVSLKELONATYFLMSLAIDM 120
 QY 68 LSAICFPFVNSVKNSTWYGTLCVIAFLVGLSCFHFAMFECISVTRYLAIA----- 124
 DB 121 LLGFLVMPVSMITLYGRMPLPSKLCVWIYLDVLFSTASIMHLCALISLDKRYAQNPI 180
 QY 125 -HHREYTKRLTEWTCIAICMVWFLSVMAFP-PVLDVGYTSFIREDOCTQHRSFRAN 182
 DB 181 HHSRFSKRAFLKITA-----WRTISVGISMPVPEGLDDSKVKEGSCCL-----AD 230
 QY 183 DSLGFMILLALILATOLVYLKIFVHDKRKKVOPVAASQNMTHFGGASQAAN 242
 DB 231 DN-FVLIGSVSPFIPLTIMVITYFL-----TKSLQKATLC-----VSDIGTRA 275
 QY 243 WLAGRCRPTPEPLIGI-----RONANTGRRRLVLDEFKMEKRISRMFYMTFL 293
 DB 276 KLASRF--LQSSLSSEKLFORSIHREPGSTTGR---TMOISNEQACVGLGIVFL 330
 QY 294 FLTMGPVIVACVYRVFAR---GPVPPGFLTAAVWMSFAQGINPFVCIFSNRELRCP 350
 DB 331 FVMMCPFITINMAVICKESCNEVIGALLNVFWIGILSSAVNPLYTLFKITRRASNF 390
 QY 351 S 351
 DB 391 S 391

RESULT 5
 US-09-292-069A-25
 ; Sequence 25, Application US/09292069A
 ; Patent No. 6140509

GENERAL INFORMATION:
 APPLICANT: Behan, Dominic P.
 APPLICANT: Chalmers, Derek T.
 APPLICANT: Foster, Richard J.
 APPLICANT: Glen, Robert C.
 APPLICANT: Lawless, Michael S.
 APPLICANT: Law, Chen W.
 APPLICANT: Liu, Qian
 APPLICANT: Russo, Joseph F.
 APPLICANT: Smith, Julian R.
 TITLE OF INVENTION: No. 6140509-Endogenous, Constitutively Activated Human
 TITLE OF INVENTION: Serotonin Receptors And Small Molecule Modulators
 TITLE OF INVENTION: Thereof
 FILE REFERENCE: AREN0033
 CURRENT APPLICATION NUMBER: US/09/292,069A.
 CURRENT FILING DATE: 1999-04-14
 PRIOR APPLICATION NUMBER: 60/090,783
 PRIOR FILING DATE: 1998-06-26
 PRIOR APPLICATION NUMBER: 60/112,909
 PRIOR FILING DATE: 1998-12-18
 PRIOR APPLICATION NUMBER: 60/123,000
 PRIOR FILING DATE: 1999-03-05
 NUMBER OF SEQ ID NOS: 33
 SOFTWARE: Patentin Ver. 2.1
 SEQ ID NO 25
 LENGTH: 470
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: NO. 6140509e1
 OTHER INFORMATION: Sequence
 US-09-292-069A-25

Query Match 13.1%; Score 258; DB 4; Length 470;
 Best Local Similarity 24.7%; Pred. No. 1,4e-15;
 Matches 89; Conservative 63; Mismatches 155; Indels 54; Gaps 12;

QY 15 LSPITAFKLTSLGF-----IIGSVVGNLLISILYKDKTLHRAVYFLLDCCSDI 67

Db 61 LSPSCSLHJOEKMSALLTAVVILLITAGNILLIVAVSLERKLOANTNVEFLMSLAIAD 120
Qy 68 LBSALCFPEVENSXKNGSWTGTGLTCKYIAFGVYSCHETAMLCISTRLAIA--- 124
Db 121 LIGFLVMPVSMILLIXGYWMPLEPSKLCAYWIDVLEFSAISIMHLAISIDRYVAIONPI 180
Qy 125 -HHREYTRKLFMTGLAVICWMTLSVMAAF-PVLDVGTYFSFIREDOCTFQHRSPRA 182
Db 181 HHSRNSRKAFKLAITA---WTTISVGISMPLVPGLODDSVFEGSCLL-----AD 230
Qy 183 DSIQGLMILLALITOLVYLKLIFFVHRRKKMPVOFAVAVSQNTFHPGASGQAAAN 242
Db 231 DN-EVLIGSFVSFPIPLITMTITVFL-----TKSIQKEATLC-----VSDGTRA 275
Qy 243 WLAGRGFTPTPLGT-----RQANNTGRRRLVLDEFKMEKRISMFTYIMTEL 293
Db 276 KLASFSF-LPOSSLSSEKLFORSIRHEGSGYGR--TMOISNEOKACKVLGIYFFL 330
Qy 294 FTLLGPIYVACYWYFAR---GPVVPGGFLTAAVMMSFAQAGINPVCIFSRRLRCF 350
Db 331 FVVMCPPEFTINIMAYCEKSCNEDVIGALLNVWIGVSSAVNPLVYTLFENKTYRSAP 390
Qy 351 S 351
Db 391 S 391

RESULT 6

US-08-570-157-7

Sequence 7, Application US/08570157

Patent No. 5750353

GENERAL INFORMATION:

APPLICANT: Koplin, Alan S.

APPLICANT: Beinborn, Martin

TITLE OF INVENTION: ASSAY FOR NON-PEPTIDE AGONISTS TO

TITLE OF INVENTION: PEPTIDE HORMONE RECEPTORS.

NUMBER OF SEQUENCES: 23

CORRESPONDENCE ADDRESS:

ADDRESS: Fish & Richardson P. C.

STREET: 225 Franklin Street

CITY: Boston

STATE: MA

COUNTRY: USA

ZIP: 02110-2804

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/570,157

FILING DATE: 11-DEC-1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Clark, Paul T.

REGISTRATION NUMBER: 30,162

REFERENCE/DOCKET NUMBER: 00398/109001

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617/542-5070

TELEFAX: 617/542-8906

TELEX: 200154

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 453 amino acids

TYPE: amino acid

STRANDEDNESS: not relevant

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-570-157-7

Query Match 13.1%; Score 257.5; DB 1; Length 453;
Best Local Similarity 24.1%; Pred. No. 1,4e-15;

Matches 91; Conservative 63; Mismatches 170; Indels 53; Gaps 9;
Qy 16 SPLTAFLKLSLGIITISVAVGNLLISILLYKOKTIHRAPIYFLDCCSILSALCFP 75
Db 64 SDLNLWARIWYSVIFLISVGNLLIIVLWNRRLRTITNSFLLSLSDLMAVAVLCP 123
Qy 76 FVF-NSVKNKSWTGTGLTCKYIAFGVYSCHETAMLCISTRYLAIAHHRYTRRL 133
Db 124 FTLLIPNIMEN--FIREVICRAAAYFMGLSVSTFNLVAISTERSAICNPLKSRWQ 180
Qy 134 TFWTGLAVICWMTLSVMAAFPPVLDVGYTSFIRE--DOCTFOHNSFRANDSLGEML 189
Db 181 TRSAAYVIAATWVLSLIMPIYVKNKYTFEPKMDRVGHQCRLYWMSKVQQA-WVYL 239
Qy 190 LLAIIILATOLVYLKLIFFVHRRKKMPVOFAVAVSQNTFHPGASGQAAANLAGEGR 249
Db 240 LTLTFLFIPGVVMI-VAAGLISRELXYGIOPEMDLNKKAHKKNGV----- 285
Qy 250 GPPPEPL-----LGIQONANTGRRRLVLDEKME-----KRISR 285
Db 286 -FTTIPSGDEGDCYIQVTKRRNTMEMSTLTPSVCTKMDPARINNSEAKLMAKRVIR 343
Qy 286 MEYIMTEFLTLMGPIYVACYWYF---ARGPVVPGGFLTAAVMMSFAQAGINPVCIFS 342
Db 344 MLIVIVAMFTICMMPFVAVNTWKAFLDELAFNTLGAIPISFHLSTYSACVNPILYCFM 403
Qy 343 NRELRCFSTLLYCRK 359
Db 404 NKRRKKAFLGTFFSSCIR 420

RESULT 7

US-09-292-071-33

Sequence 33, Application US/09292071

Patent No. 6107324

GENERAL INFORMATION:

APPLICANT: Behan, Dominic

APPLICANT: Chalmers, Derick

TITLE OF INVENTION: No. 6107324-Endogenous, Constitutively Activated

TITLE OF INVENTION: Human Serotonin Receptors and Small Molecule Modulators Th

NUMBER OF SEQUENCES: 33

CORRESPONDENCE ADDRESS:

ADDRESS: Arena Pharmaceuticals, Inc.

STREET: 6166 Nancy Ridge Drive

CITY: San Diego

STATE: CA

COUNTRY: USA

ZIP: 92121

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/292,071

FILING DATE: April 14, 1999

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Mark J. Rosen

REGISTRATION NUMBER: 39,822

TELECOMMUNICATION INFORMATION:

TELEPHONE: (215) 564-6525

TELEFAX: (215) 568-3439

INFORMATION FOR SEQ ID NO: 33:

SEQUENCE CHARACTERISTICS:

LENGTH: 478 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: not relevant

MOLECULE TYPE: protein

US-09-292-071-33

Query Match 13.1%; Score 256.5; DB 3; Length 478;
Best Local Similarity 23.9%; Pred. No. 1.9e-15;
Matches 83; Conservative 64; Mismatches 150; Indels 51; Gaps 11;

QY 30 IIVSVVGNLLISLIVKDKTLHRAPIYFLDLCCSDILSAICFPFVNSVKNSTWY 89
DB 84 VILITLAINLIVMAVSEKKNATNTVFLMSLAIDMLGLVMPVSMITLITGYRML 143
QY 90 GLTLCVIAFLVLCSCFTAFMLFCISVTRYLAIA-----HREYTKLTFMTCLAVICW 145
DB 144 PSKLCAMVILDLVLPSTASIMHLCASLDRVAIAQNPISHRSNSTRKAFKIIA-----V 199
QY 146 WLSVMAAP-PVLDVGYTSFIREDOCTFOHRSFRANDS-IGFMILLALILATOL-VY 202
DB 200 WTISVGSIMPIVFGLODDSKVFKESGLLADNDFVLIGSVSFPIITIMVITYCLTIT 259
QY 203 L--KLIFVHDKRKKMP---VOFVAASONTFHPGASGQAANWLAGFGGPTPTL 256
DB 260 VLRRQALMLHGHTEEPGLSLDFLKCKRN-----TAEENSAN----- 299
QY 257 LGIRONANTGRRRL-----VLDEFKMERISRMFYIMFLFLIMGPYLVACYRW 309
DB 300 ---PNODNARRKKRRPRTGMOAINNERKAKVIGIVFVFLIMCPFITINIAV 355

QY 310 FAR---GPVVGGLTAAYVMSFAQAGINPFVCIFSNRELRCFSTTL 354
DB 356 ICKESCNEDVIGALLNVFWIGILSSAVNPVLTLEFKITRRAFSNYL 403

RESULT 8
US-09-292-069A-33
Sequence 33, Application US/09292069A
Patent No. 6140509
GENERAL INFORMATION:
APPLICANT: Behan, Dominic P
APPLICANT: Chalmers, Derek T
APPLICANT: Foster, Richard J
APPLICANT: Glen, Robert C
APPLICANT: Lawless, Michael S
APPLICANT: Liaw, Chen W
APPLICANT: Liu, Qian
APPLICANT: Russo, Joseph F
APPLICANT: Smith, Julian R
APPLICANT: Thomson, William J
TITLE OF INVENTION: No. 6140509-Endogenous, Constitutively Activated Human
TITLE OF INVENTION: Serotonin Receptors And Small Molecule Modulators
FILE REFERENCE: AREN0033
CURRENT APPLICATION NUMBER: US/09/292,069A
CURRENT FILING DATE: 1999-04-14
PRIOR APPLICATION NUMBER: 60/090,783
PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/112,909
PRIOR FILING DATE: 1998-12-18
PRIOR APPLICATION NUMBER: 60/123,000
PRIOR FILING DATE: 1999-03-05
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 33
LENGTH: 478
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: No. 6140509e1
US-09-292-069A-33

Query Match 13.1%; Score 256.5; DB 4; Length 478;
Best Local Similarity 23.9%; Pred. No. 1.9e-15;
Matches 83; Conservative 64; Mismatches 150; Indels 51; Gaps 11;

QY 30 IIGVSVGNLLISLIVKDKTLHRAPIYFLDLCCSDILSAICFPFVNSVKNSTWY 89

DB 84 VILITLAINLIVMAVSEKKNATNTVFLMSLAIDMLGLVMPVSMITLITGYRML 143
QY 90 GLTLCVIAFLVLCSCFTAFMLFCISVTRYLAIA-----HREYTKLTFMTCLAVICW 145
DB 144 PSKLCAMVILDLVLPSTASIMHLCASLDRVAIAQNPISHRSNSTRKAFKIIA-----V 199
QY 146 WLSVMAAP-PVLDVGYTSFIREDOCTFOHRSFRANDS-IGFMILLALILATOL-VY 202
DB 200 WTISVGSIMPIVFGLODDSKVFKESGLLADNDFVLIGSVSFPIITIMVITYCLTIT 259
QY 203 L--KLIFVHDKRKKMP---VOFVAASONTFHPGASGQAANWLAGFGGPTPTL 256
DB 260 VLRRQALMLHGHTEEPGLSLDFLKCKRN-----TAEENSAN----- 299
QY 257 LGIRONANTGRRRL-----VLDEFKMERISRMFYIMFLFLIMGPYLVACYRW 309
DB 300 ---PNODNARRKKRRPRTGMOAINNERKAKVIGIVFVFLIMCPFITINIAV 355

QY 310 FAR---GPVVGGLTAAYVMSFAQAGINPFVCIFSNRELRCFSTTL 354
DB 356 ICKESCNEDVIGALLNVFWIGILSSAVNPVLTLEFKITRRAFSNYL 403

RESULT 9
US-08-118-270-19
Sequence 19, Application US/08118270
Patent No. 5508384
GENERAL INFORMATION:
APPLICANT: Murphy, Randall B.
APPLICANT: Schuster, David I.
TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
NUMBER OF SEQUENCES: 348
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/118,270
FILING DATE: 09-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/943,236
FILING DATE: 10-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Townsend, Kevin G.
REGISTRATION NUMBER: 34,033
REFERENCE/DOCKET NUMBER: MURPHY-2A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 330 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-118-270-19

Query Match 13.0%; Score 255; DB 1; Length 330;
Best Local Similarity 25.3%; Pred. No. 1.7e-15;
Matches 89; Conservative 60; Mismatches 153; Indels 50; Gaps 13;

QY 27 LGFTIGSVGNLLISILVNDKTLHRAFYFLDLCCSDILRSALCFEPVNSVKN-S 85
DB 8 VGFLLVTVGNLVIAVLTSTRALRAPQNLVLSIASADILVATLMPF---SLANEIM 64
QY 86 TWYGTCTCKVIAFLVSCFHTAFMLFCISVTRYLAIHHRRYTKRLFTWTCIAVICW 145
DB 65 YWYFGQWCGVYLAIDVLCFTSSIVHLCALSDRYSVQAVEYLNKRTPRRKATIVAV 124
QY 146 WLSVMAAPFPVLDVGTYSFIRED---OCTFOHRS-FRANSLGFMILLALILALATO 199
DB 125 WLSAVISFPLV-----SLYROPDGAAPQCGINDETWYILSSCIGSFAPCLILY--- 176
QY 200 LVYKLIFVHNR-----KMKPVQFVAVSQNTFHGPGASQAANWL---AGCGRG 250
DB 177 LVYAR-IYRAKRRRTLTSEKRAV-----GPDGASPTTENGIGAAAGART 222
QY 251 PTPPLTIGIQNANTGRRRLVLDERKMKRISRMFYIMTFLTLMP-YLVACYWYV 309
DB 223 GTARFLSRRRRRASSVCRRK-----AQAEREFTFVALVLCWPFFFIYSLXGI 275
QY 310 FARGPVPGGFLTAAVWMSFAQGINPVCIFSNRELRCFSTLLCYCRSR 361
DB 276 CREACQVGPGLFKEFFWIGYCNSLNPVITYVFNQDPRSPK-HILFRRRRR 326

RESULT 10

PCT-US93-08528-19

Sequence 19, Application PC/TUS9308528

GENERAL INFORMATION:

APPLICANT: New York University

TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN

TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF

NUMBER OF SEQUENCES: 348

CORRESPONDENCE ADDRESS:

ADDRESS: BROWDY AND NEWMARK

STREET: 419 Seventh Street, N.W., Suite 300

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US93/08528

FILING DATE: 09-SEP-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/943,236

FILING DATE: 10-SEP-1992

ATTORNEY/AGENT INFORMATION:

NAME: Townsend, Kevin G.

REGISTRATION NUMBER: 34,033

REFERENCE/DOCKET NUMBER: MORPHY-2 PCT

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-628-5197

TELEFAX: 202-737-3528

TELEX: 248633

INFORMATION FOR SEQ ID NO: 19:

SEQUENCE CHARACTERISTICS:

LENGTH: 330 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

PCT-US93-08528-19

Query Match 13 0%; Score 255; DB 5; Length 330;
Best Local Similarity 25.3%; Pred. No. 1,7e-15;
Matches 89; Conservative 60; Mismatches 153; Indels 50; Gaps 13;

QY 27 LGFTIGSVGNLLISILVNDKTLHRAFYFLDLCCSDILRSALCFEPVNSVKN-S 85
DB 8 VGFLLVTVGNLVIAVLTSTRALRAPQNLVLSIASADILVATLMPF---SLANEIM 64
QY 86 TWYGTCTCKVIAFLVSCFHTAFMLFCISVTRYLAIHHRRYTKRLFTWTCIAVICW 145
DB 65 YWYFGQWCGVYLAIDVLCFTSSIVHLCALSDRYSVQAVEYLNKRTPRRKATIVAV 124
QY 146 WLSVMAAPFPVLDVGTYSFIRED---OCTFOHRS-FRANSLGFMILLALILALATO 199
DB 125 WLSAVISFPLV-----SLYROPDGAAPQCGINDETWYILSSCIGSFAPCLILY--- 176
QY 200 LVYKLIFVHNR-----KMKPVQFVAVSQNTFHGPGASQAANWL---AGCGRG 250
DB 177 LVYAR-IYRAKRRRTLTSEKRAV-----GPDGASPTTENGIGAAAGART 222
QY 251 PTPPLTIGIQNANTGRRRLVLDERKMKRISRMFYIMTFLTLMP-YLVACYWYV 309
DB 223 GTARFLSRRRRRASSVCRRK-----AQAEREFTFVALVLCWPFFFIYSLXGI 275
QY 310 FARGPVPGGFLTAAVWMSFAQGINPVCIFSNRELRCFSTLLCYCRSR 361
DB 276 CREACQVGPGLFKEFFWIGYCNSLNPVITYVFNQDPRSPK-HILFRRRRR 326

RESULT 11

US-07-817-920-8

Sequence 8, Application US/07817920

Patent No. 5360735

GENERAL INFORMATION:

APPLICANT: Weinshank, Richard L

APPLICANT: Branchek, Theresa

TITLE OF INVENTION: DNA ENCODING A HUMAN 5-HT1F RECEPTOR AND

NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:

ADDRESS: Cooper & Dunham

STREET: 30 Rockefeller Plaza

CITY: New York

STATE: New York

COUNTRY: USA

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/817,920

FILING DATE: 19920108

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: White, John P

REGISTRATION NUMBER: 28,678

REFERENCE/DOCKET NUMBER: 1795/39318

TELECOMMUNICATION INFORMATION:

TELEPHONE: 212-977-9550

TELEFAX: 212-664-0525

TELEX: 422523 COOP UI

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 471 amino acids

TYPE: AMINO ACID

STRANDEDNESS: unknown

TOPOLOGY: linear

MOLECULE TYPE: protein

HYPOTHETICAL: NO

ANTI-SENSE: NO

FRAGMENT TYPE: N-terminal

IMMEDIATE SOURCE:

CLONE: 5-HT2

US-07-817-920-8

Query Match	12.98;	Score 253.5;	DB 1;	Length 471;
Best Local Similarity	24.88;	Pred. No. 3.4e-15;		
Matches	84;	Conservative	61;	Mismatches 147;
			Indels	47;
			Gaps	11.

[illegible]

RESULT 12
US-08-370-542-7

; Sequence 7, Application US/08370542
; Patent No. 5476782

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? SEQUENCE CHARACTERISTICS:
? LENGTH: 471 amino acids
? type: amino acid
? STRANDEDNESS: unknown
? TOPOLOGY: unknown
? MOLECULE TYPE: protein
? HYPOTHETICAL: NO
? ANTI-SENSE: NO
? FRAGMENT TYPE: N-terminal
US-08-370-542-7

```

Query Match	12.9%	Score 253.5;	DB 1;	Length 471;
Best Local Similarity	24.8%	Pred. No. 3,4e-15		
Matches	84;	Conservative	61;	Mismatches 147;
				Indels 47;
				Gaps 11

```

0Y  30 IIGSVONNLLISLIVYDKFLHAPYFLDLDCSDLSRAICFPPYVNSVKNGSMTY  89
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db  84 VIILTIAGNIIIVMAVSEIKLOQNTNTFLMSLADMLGELVMPYSMILITLYGYMPL 143
0Y  90 GLTCKVYAFVLGVLSCEFTTAMLEFCISVTRYLATA---HHREYTKRLTEWTCVAVCM 145
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db  144 PSKLCVAVITLDVLEFSTASIMHLCALSDIRVVALQONPHHSRFRMSRKAFKLIA-----V 199
0Y  146 WTLVSAVMAFP-PVLVDGYTYSFIREDDCCTQOHSFRANDSIGFMLLALILATQVLYLK 204
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Db  200 WTISVIGMSPRPVFGLODDSKVFRREGSCLL-----ADDN--FVLISFVSFFILPIITMV 251
0Y  205 LIFPVHRRKKKKRPQVFAVANSQNNWTFHFGPAGSAGQAAANMLAGFCRGPTPLLGI----- 255
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db  252 ITYFL-----TIKSLOKEATLC-----VSDIGTRAKLASFSF--LPDSSISEKILQ 296
0Y  260 -----RQANNTGRRRLVLDEFKMEKRISRMFYIMTFLFLTLMGPIYLVACTWYRFAR--- 312
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db  297 RSIHREPOSTYGR--TMOISINEOKACKVGLIVFELVVMCMCPFITNIMAYICKESC 353
0Y  313 GPVVPGGFLTAAYMNSFAQAGINPVCVJFSRRELRPOCS 351
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Db  354 NEDVIGALLANFVWIGYSSAVNPLVYTLLEKTKYRSAPS 392

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RESULT 13
US-08-117-006-8

; Sequence 8, Application US/08117006
; Patent No. 5639652

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TELEPHONE: 212-977-9550
TELEFAX: 212-664-0525
TELEX: 422523 COOP UI
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 471 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
IMMEDIATE SOURCE:
CLONE: 5-HT2
US-08-117-006-8

Query Match 12.9%; Score 253.5; DB 1; Length 471;
Best Local Similarity 24.8%; Pred. No. 3.4e-15;
Matches 84; Conservative 61; Mismatches 147; Indels 47; Gaps 11;

QY 30 IIGSVVGNLLISILVKKDKTHRAPYFLLDCCSDILRSALCPFFVNSVNGSTWTY 89
DB 84 VILITAGNIIIVMAVSLERKLNATNFTLSLADMLGLFVMPVSMILTYGYRMP 143
QY 90 GLTCKVIAFLGLVSCFHTAFMLFCISVTRYLAIA---HHREYTKRLTFWTCIAVICW 145
DB 144 PSKLCAMVYLDVLFSTASIMHLCALSLDRVVAIONPIHHSRNSRKAKLKIITA---V 199
QY 146 WTLVSAMAF-PVLDVGYTSFIREDOCTFOHRSFRANDSLGFMILLALILLATQVLYLK 204
DB 200 WTLISVGISMPIPVGLDDSKVFEKGSCLL-----ADDN--FVLISFVSFFPLITIMV 251
QY 205 LIFFVDRKKMPVQFAVAASQNTFHGPGASGQAANWLAGFGRGPTPLTIGI----- 259
DB 252 ITYFL---TISLQKENTLC-----VSDLGTRAKLASFS--LPQSSLSSEKLFQ 296
QY 260 ---RQANNTGRRLLVLDEFKMEKRISRMFYIMTFLTLGMPYLACVYRWYFAR--- 312
DB 297 RSIHREPGSYTGR---TMQISINEQKACKVIGIVFLEFVVMCPFTITINMAVICRSC 353
QY 313 GPVVGGLTAAVWMSFPAQAGINPVCIFSNRELRCFS 351
DB 354 NEDVIGALLNVFWIGYLSAVNPVLYTLFKNKTYRSAFS 392

RESULT 14
US-08-216-594-8
Sequence 8, Application US/08216594
Patent No. 5652113

GENERAL INFORMATION:

APPLICANT: Weinsbank, Richard L.
APPLICANT: Branchek, Theresa
APPLICANT: Hartig, Paul R.
TITLE OF INVENTION: DNA ENCODING A HUMAN 5-HT1F RECEPTOR
TITLE OF INVENTION: AND USES THEREOF
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
COUNTRY: USA

ZIP: 10112

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/216,594
FILING DATE:

CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 1795/39318
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-977-9550
TELEFAX: 212-664-0525

TELEX: 422523 COOP UI
INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 471 amino acids

TYPE: amino acid

STRANDEDNESS: unknown

TOPOLOGY: linear

MOLECULE TYPE: protein

HYPOTHETICAL: NO

ANTI-SENSE: NO

FRAGMENT TYPE: N-terminal

IMMEDIATE SOURCE:

CLONE: 5-HT2
US-08-216-594-8

Query Match 12.9%; Score 253.5; DB 1; Length 471;
Best Local Similarity 24.8%; Pred. No. 3.4e-15;
Matches 84; Conservative 61; Mismatches 147; Indels 47; Gaps 11;

QY 30 IIGSVVGNLLISILVKKDKTHRAPYFLLDCCSDILRSALCPFFVNSVNGSTWTY 89
DB 84 VILITAGNIIIVMAVSLERKLNATNFTLSLADMLGLFVMPVSMILTYGYRMP 143
QY 90 GLTCKVIAFLGLVSCFHTAFMLFCISVTRYLAIA---HHREYTKRLTFWTCIAVICW 145
DB 144 PSKLCAMVYLDVLFSTASIMHLCALSLDRVVAIONPIHHSRNSRKAKLKIITA---V 199
QY 146 WTLVSAMAF-PVLDVGYTSFIREDOCTFOHRSFRANDSLGFMILLALILLATQVLYLK 204
DB 200 WTLISVGISMPIPVGLDDSKVFEKGSCLL-----ADDN--FVLISFVSFFPLITIMV 251
QY 205 LIFFVDRKKMPVQFAVAASQNTFHGPGASGQAANWLAGFGRGPTPLTIGI----- 259
DB 252 ITYFL---TISLQKENTLC-----VSDLGTRAKLASFS--LPQSSLSSEKLFQ 296
QY 260 ---RQANNTGRRLLVLDEFKMEKRISRMFYIMTFLTLGMPYLACVYRWYFAR--- 312
DB 297 RSIHREPGSYTGR---TMQISINEQKACKVIGIVFLEFVVMCPFTITINMAVICRSC 353
QY 313 GPVVGGLTAAVWMSFPAQAGINPVCIFSNRELRCFS 351
DB 354 NEDVIGALLNVFWIGYLSAVNPVLYTLFKNKTYRSAFS 392

RESULT 15
US-08-542-358-7
Sequence 7, Application US/08542358
Patent No. 5786155

GENERAL INFORMATION:

APPLICANT: Weinsbank, Richard L.
APPLICANT: Branchek, Theresa
APPLICANT: Hartig, Paul R.
TITLE OF INVENTION: DNA ENCODING A HUMAN 5-HT1E RECEPTOR AND USES THEREOF
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.

ZIP: 10036

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/542,358
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 1795/39317-22/JPM/MAT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-278-0400
TELEFAX: 212-391-0525
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 471 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
US-08-542-358-7

Query Match 12.9%; Score 253.5; DB 1; Length 471;

Best Local Similarity 24.8%; Pred. No. 3,4e-15;
Matches 84; Conservative 61; Mismatches 147; Indels 47; Gaps 11;

OY 30 IIGVGVGGLLSILLVKPTLHRAVYPLLDCCSDILRSALCPFVFNVSXNGSTWY 89
DB 84 VILLIAGNILLIMAVSEKLLQNNATNYFLMSLAIDMLGLVMPVSMILLYGRWPL 143
OY 90 GLTCKVIAFLGVLSCFHTAFMLFCISVRYLAIA---HHRFYTRLFETCLAVICWY 145
DB 144 PSKLCVWYLDVLFSTASIMLCALSDRYAIONPIHHSRNSXTKAFLKIIA---V 199
OY 146 WLSYVMAFP-PVLGVGYSTFIREDQCTFQHSFRANDSLGFMILLALLATOLVLYK 204
DB 200 WTISVIGISMPLEVFGLQDSKVEKESCLL-----ADDN--FVLIGSFVSFPLTIWY 251
OY 205 LIFFVHDRKKMPVQFVAVSONWTFHGGASGQAANMLAGRGKPTPTLLGI----- 259
DB 252 IITYFL---TISLQKEATLC-----VSDIGTRAKLASFSF--LPSSLSSEKLFQ 296
OY 260 ---RQNNNTGRRLVLYDEFKMERKISRMFYIMTFLITLNGPYLVACYWRVPAR--- 312
DB 297 RSIHREPGSYTERR---TWQSTISNEKACKVLAGIYFFLVVMWCPFTINIMAVICKESC 353
OY 313 GPVVGGEFLTAAVWMSFAQAGINPFVCIPSNRELRCFS 351
DB 354 NEDVIGALLNVEWIGILSSAVNPLVYTLFNKTYRGAFS 392

Search completed: July 19, 2002, 14:39:37
Job time: 158 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OK protein - protein search, using sw model

Run on: July 19, 2002, 14:38:44 ; Search time 110.32 Seconds

(without alignments)
1180.500 Million cell updates/sec

Title: US-09-698-419-14

Perfect score: 1963
1 MANYSHADN1LONLSPLETA.....STLLYCRKSLPREPYCVI 370

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 3502263 seqs, 351980561 residues

Total number of hits satisfying chosen parameters: 3502263

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Pending_Patents_AA_Main:*

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	1963	100.0	370	15	US-09-145-745-1
2	1963	100.0	370	16	US-09-264-041-2
3	1963	100.0	370	17	US-09-383-745-1
4	1963	100.0	370	18	US-09-416-760-28
5	1963	100.0	370	18	US-09-416-760A-28
6	1963	100.0	370	18	US-09-417-044-26
7	1963	100.0	370	18	US-09-427-653-2

8	1963	100.0	370	19	US-09-544-254-2	Sequence 2, Appl1
9	1963	100.0 <td>370</td> <td>20</td> <td>US-09-622-439-4</td> <td>Sequence 4, Appl1</td>	370	20	US-09-622-439-4	Sequence 4, Appl1
10	1963	100.0 <td>370</td> <td>20</td> <td>US-09-622-439-24</td> <td>Sequence 24, Appl1</td>	370	20	US-09-622-439-24	Sequence 24, Appl1
11	1963	100.0 <td>370</td> <td>20</td> <td>US-09-698-419-14</td> <td>Sequence 14, Appl1</td>	370	20	US-09-698-419-14	Sequence 14, Appl1
12	1963	100.0 <td>370</td> <td>20</td> <td>US-09-875-076-26</td> <td>Sequence 26, Appl1</td>	370	20	US-09-875-076-26	Sequence 26, Appl1
13	1963	100.0 <td>370</td> <td>22</td> <td>US-09-876-252-28</td> <td>Sequence 28, Appl1</td>	370	22	US-09-876-252-28	Sequence 28, Appl1
14	1963	100.0 <td>370</td> <td>23</td> <td>US-09-888-922-16</td> <td>Sequence 16, Appl1</td>	370	23	US-09-888-922-16	Sequence 16, Appl1
15	1963	100.0 <td>370</td> <td>24</td> <td>US-10-043-943-2</td> <td>Sequence 2, Appl1</td>	370	24	US-10-043-943-2	Sequence 2, Appl1
16	1963	100.0 <td>376</td> <td>1</td> <td>PCT-US99-08605-2</td> <td>Sequence 79, Appl1</td>	376	1	PCT-US99-08605-2	Sequence 79, Appl1
17	1963	100.0 <td>379</td> <td>24</td> <td>US-10-073-885-79</td> <td>Sequence 3, Appl1</td>	379	24	US-10-073-885-79	Sequence 3, Appl1
18	1963	100.0 <td>379</td> <td>24</td> <td>US-10-031-904-3</td> <td>Sequence 1178, Appl1</td>	379	24	US-10-031-904-3	Sequence 1178, Appl1
19	1959	99.8	370	26	US-60-145-232-3	Sequence 22, Appl1
20	1959	99.8	370	26	US-60-248-505-1178	Sequence 20, Appl1
21	1790.5	91.2	373	18	US-09-416-760-22	Sequence 20, Appl1
22	1288.5	65.6	373	18	US-09-416-760A-18	Sequence 18, Appl1
23	1288.5	65.6	373	18	US-09-417-044-20	Sequence 2, Appl1
24	1288.5	65.6	373	22	US-09-875-076-20	Sequence 2, Appl1
25	1288.5	65.6	373	22	US-09-876-252-22	Sequence 2, Appl1
26	1288.5	65.6	373	1	PCT-US00-30541-2	Sequence 453, Appl1
27	1283.5	65.4	373	18	US-09-433-840-2	Sequence 77, Appl1
28	1283.5	65.4	373	20	US-09-622-439-6	Sequence 26, Appl1
29	1283.5	65.4	373	16	US-09-277-398-2	Sequence 2, Appl1
30	1283.5	65.4	373	26	US-60-213-844-453	Sequence 2, Appl1
31	1283.5	65.4	378	1	PCT-US01-01310-77	Sequence 1, Appl1
32	1283.5	65.4	378	24	US-10-073-885-77	Sequence 2, Appl1
33	1276.5	65.0	373	20	US-09-622-439-26	Sequence 2, Appl1
34	1274.5	64.9	373	1	PCT-US99-08576-2	Sequence 2, Appl1
35	1274.5	64.9	373	16	US-09-277-398-2	Sequence 2, Appl1
36	1274.5	64.9	373	16	US-09-760-354A-2	Sequence 1, Appl1
37	1270.5	64.7	373	16	US-09-200-302-1	Sequence 1, Appl1
38	998.5	50.9	375	17	US-09-321-636-2	Sequence 18, Appl1
39	998.5	50.9	375	18	US-09-416-760-18	Sequence 18, Appl1
40	998.5	50.9	375	18	US-09-416-760A-18	Sequence 16, Appl1
41	998.5	50.9	375	18	US-09-417-044-16	Sequence 2, Appl1
42	998.5	50.9	375	20	US-09-622-439-2	Sequence 2, Appl1
43	998.5	50.9	375	20	US-09-634-392-1	Sequence 16, Appl1
44	998.5	50.9	375	22	US-09-875-076-16	Sequence 18, Appl1
45	998.5	50.9	375	22	US-09-876-252-18	Sequence 18, Appl1

ALIGNMENTS

RESULT 1

US-09-145-745-1

Sequence 1, Application US/09145745A

GENERAL INFORMATION:

APPLICANT: Glucksmann, Maria A.

TITLE OF INVENTION: 14926 Receptor, A Novel G-Protein Coupled Receptor

FILE REFERENCE: 035800/169197

CURRENT APPLICATION NUMBER: US/09/145,745A

CURRENT FILING DATE: 1998-09-02

NUMBER OF SEQ ID NOS: 3

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 1

LENGTH: 370

TYPE: PRT

ORGANISM: Homo sapiens

US-09-145-745-1

Query Match 100.0%; Score 1963; DB 15; Length 370;
Best Local Similarity 100.0%; Pred. No. 4.6e-182;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB	1	MANYSHADN1LONLSPLETAFLKLTISGLFTIGSVGNLISILVVDKTLHRAAPYFLL 60
QY	61	DLCCSDILRAICFPFFVNSVKNSTWTGTLCKVIAFLGVLSCHTFAPMLFISTVRY 120
DB	61	DLCCSDILRAICFPFFVNSVKNSTWTGTLCKVIAFLGVLSCHTFAPMLFISTVRY 120

OY 121 LAIAHHRFTYKRLTFWTCIAVICMWTLSVMAAFPPVLDVGTYSFIREDOCTFOHRSFR 180
DB 121 LAIAHHRFTYKRLTFWTCIAVICMWTLSVMAAFPPVLDVGTYSFIREDOCTFOHRSFR 180
OY 181 ANDSLGFMILLALILATOLVYLKLFVYHRRKMKPVQFAVAASQWTFHGPCASGQAA 240
DB 181 ANDSLGFMILLALILATOLVYLKLFVYHRRKMKPVQFAVAASQWTFHGPCASGQAA 240
OY 241 ANMLAGFGGPTPTLLGIRONANTTGRRLVLDEFKMKRISRMFYIMTFLETLTMDP 300
DB 241 ANMLAGFGGPTPTLLGIRONANTTGRRLVLDEFKMKRISRMFYIMTFLETLTMDP 300
OY 301 YIVACYWRVFAAGPVVGGFLTAAVMMSFAQAGINPVCIFSNRELRCRCESTLLYCRKS 360
DB 301 YIVACYWRVFAAGPVVGGFLTAAVMMSFAQAGINPVCIFSNRELRCRCESTLLYCRKS 360
OY 361 RLPREPYCVI 370
DB 361 RLPREPYCVI 370

RESULT 2

US-09-264-041-2
Sequence 2, Application US/09264041
GENERAL INFORMATION:
APPLICANT: Smith, Kelli E.
APPLICANT: Pathirana, Marie Sudam
APPLICANT: Kyaw, Hla
APPLICANT: Borowsky, Beth E.
TITLE OF INVENTION: DNA ENCODING ORPHAN SNORF12 RECEPTOR
FILE REFERENCE: 58801
CURRENT APPLICATION NUMBER: US/09/264,041
CURRENT FILING DATE: 1999-03-08
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.0 - beta
SEQ ID NO 2
LENGTH: 370
TYPE: PRT
ORGANISM: Homo sapiens
US-09-264-041-2

Query Match 100.0%; Score 1963; DB 16; Length 370;
Best Local Similarity 100.0%; Pred. No. 4, 6e-182;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MANYSHADNILONLSPLTAFLKLTSLGFTIGSVGNLLISILVYDKTLHRAPIYFEL 60
OY 61 DLCCSDILRSALCFEPFVNSVKNSTWYGTLCCKVIAFLGVLSCFHTAFMLFCISVTRY 120
DB 61 DLCCSDILRSALCFEPFVNSVKNSTWYGTLCCKVIAFLGVLSCFHTAFMLFCISVTRY 120
OY 121 LAIAHHRFTYKRLTFWTCIAVICMWTLSVMAAFPPVLDVGTYSFIREDOCTFOHRSFR 180
DB 121 LAIAHHRFTYKRLTFWTCIAVICMWTLSVMAAFPPVLDVGTYSFIREDOCTFOHRSFR 180
OY 181 ANDSLGFMILLALILATOLVYLKLFVYHRRKMKPVQFAVAASQWTFHGPCASGQAA 240
DB 181 ANDSLGFMILLALILATOLVYLKLFVYHRRKMKPVQFAVAASQWTFHGPCASGQAA 240
OY 241 ANMLAGFGGPTPTLLGIRONANTTGRRLVLDEFKMKRISRMFYIMTFLETLTMDP 300
DB 241 ANMLAGFGGPTPTLLGIRONANTTGRRLVLDEFKMKRISRMFYIMTFLETLTMDP 300
OY 301 YIVACYWRVFAAGPVVGGFLTAAVMMSFAQAGINPVCIFSNRELRCRCESTLLYCRKS 360
DB 301 YIVACYWRVFAAGPVVGGFLTAAVMMSFAQAGINPVCIFSNRELRCRCESTLLYCRKS 360
OY 361 RLPREPYCVI 370
DB 361 RLPREPYCVI 370

RESULT 3

US-09-383-745-1
Sequence 1, Application US/09383745
GENERAL INFORMATION:
APPLICANT: Glucksmann, Maria A.
TITLE OF INVENTION: 14926 Receptor, A Novel G-Protein Coupled Receptor
FILE REFERENCE: 035800/169197
CURRENT APPLICATION NUMBER: US/09/383,745
CURRENT FILING DATE: 1999-08-26
PRIOR APPLICATION NUMBER: 09/145,745
PRIOR FILING DATE: 1998-09-02
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 370
TYPE: PRT
ORGANISM: Homo sapiens
US-09-383-745-1

Query Match 100.0%; Score 1963; DB 17; Length 370;
Best Local Similarity 100.0%; Pred. No. 4, 6e-182;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MANYSHADNILONLSPLTAFLKLTSLGFTIGSVGNLLISILVYDKTLHRAPIYFEL 60
DB 1 MANYSHADNILONLSPLTAFLKLTSLGFTIGSVGNLLISILVYDKTLHRAPIYFEL 60
OY 61 DLCCSDILRSALCFEPFVNSVKNSTWYGTLCCKVIAFLGVLSCFHTAFMLFCISVTRY 120
DB 61 DLCCSDILRSALCFEPFVNSVKNSTWYGTLCCKVIAFLGVLSCFHTAFMLFCISVTRY 120
OY 121 LAIAHHRFTYKRLTFWTCIAVICMWTLSVMAAFPPVLDVGTYSFIREDOCTFOHRSFR 180
DB 121 LAIAHHRFTYKRLTFWTCIAVICMWTLSVMAAFPPVLDVGTYSFIREDOCTFOHRSFR 180
OY 181 ANDSLGFMILLALILATOLVYLKLFVYHRRKMKPVQFAVAASQWTFHGPCASGQAA 240
DB 181 ANDSLGFMILLALILATOLVYLKLFVYHRRKMKPVQFAVAASQWTFHGPCASGQAA 240
OY 241 ANMLAGFGGPTPTLLGIRONANTTGRRLVLDEFKMKRISRMFYIMTFLETLTMDP 300
DB 241 ANMLAGFGGPTPTLLGIRONANTTGRRLVLDEFKMKRISRMFYIMTFLETLTMDP 300
OY 301 YIVACYWRVFAAGPVVGGFLTAAVMMSFAQAGINPVCIFSNRELRCRCESTLLYCRKS 360
DB 301 YIVACYWRVFAAGPVVGGFLTAAVMMSFAQAGINPVCIFSNRELRCRCESTLLYCRKS 360
OY 361 RLPREPYCVI 370
DB 361 RLPREPYCVI 370

RESULT 4

US-09-416-760-28
Sequence 28, Application US/09416760
GENERAL INFORMATION:
APPLICANT: Behan, Dominic P.
APPLICANT: Lehmann-Bruinsma, Karin
APPLICANT: Chalmers, Derek T.
APPLICANT: Lowitz, Kevin P.
APPLICANT: Lin, I-Tsin
APPLICANT: Dang, Huong T.
APPLICANT: Chen, Ruoping
APPLICANT: Liaw, Chen W.
TITLE OF INVENTION: Non-Endogenous Constitutively Activated Human G Protein Coupled
FILE REFERENCE: AREN-0054
CURRENT APPLICATION NUMBER: US/09/416,760
CURRENT FILING DATE: 1999-10-12
PRIOR APPLICATION NUMBER: 09/170,496
PRIOR FILING DATE: 1998-10-13

PRIOR APPLICATION NUMBER: 60/110,060
 PRIOR FILING DATE: 1998-11-27
 PRIOR APPLICATION NUMBER: 60/120,416
 PRIOR FILING DATE: 1999-02-16
 PRIOR APPLICATION NUMBER: 60/121,852
 PRIOR FILING DATE: 1999-02-26
 PRIOR APPLICATION NUMBER: 60/109,213
 PRIOR FILING DATE: 1998-11-20
 PRIOR APPLICATION NUMBER: 60/123,944
 PRIOR FILING DATE: 1999-03-12
 PRIOR APPLICATION NUMBER: 60/123,945
 PRIOR FILING DATE: 1999-03-12
 PRIOR APPLICATION NUMBER: 60/123,948
 PRIOR FILING DATE: 1999-03-12
 PRIOR APPLICATION NUMBER: 60/123,951
 PRIOR FILING DATE: 1999-03-12
 PRIOR APPLICATION NUMBER: 60/123,946
 PRIOR FILING DATE: 1999-03-12
 PRIOR APPLICATION NUMBER: 60/123,949
 PRIOR FILING DATE: 1999-03-12
 PRIOR APPLICATION NUMBER: 60/152,524
 PRIOR FILING DATE: 1999-09-03
 PRIOR APPLICATION NUMBER: 60/151,114
 PRIOR FILING DATE: 1999-08-27
 PRIOR APPLICATION NUMBER: 60/108,029
 PRIOR FILING DATE: 1998-11-12
 PRIOR APPLICATION NUMBER: 60/136,436
 PRIOR FILING DATE: 1999-05-28
 PRIOR APPLICATION NUMBER: 60/136,439
 PRIOR FILING DATE: 1999-05-28
 PRIOR APPLICATION NUMBER: 60/136,567
 PRIOR FILING DATE: 1999-05-28
 PRIOR APPLICATION NUMBER: 60/137,127
 PRIOR FILING DATE: 1999-05-28
 PRIOR APPLICATION NUMBER: 60/137,131
 PRIOR FILING DATE: 1999-05-28
 PRIOR APPLICATION NUMBER: 60/141,448
 PRIOR FILING DATE: 1999-06-29
 PRIOR APPLICATION NUMBER: 60/136,437
 PRIOR FILING DATE: 1999-05-28
 PRIOR APPLICATION NUMBER: 60/156,555
 PRIOR FILING DATE: 1999-09-29
 PRIOR APPLICATION NUMBER: 60/156,634
 PRIOR FILING DATE: 1999-09-29
 PRIOR APPLICATION NUMBER: 60/156,653
 PRIOR FILING DATE: 1999-09-29
 PRIOR APPLICATION NUMBER: 60/157,280
 PRIOR FILING DATE: 1999-10-01
 PRIOR APPLICATION NUMBER: 60/157,294
 PRIOR FILING DATE: 1999-10-01
 PRIOR APPLICATION NUMBER: 60/157,281
 PRIOR FILING DATE: 1999-10-01
 PRIOR APPLICATION NUMBER: 60/157,282
 PRIOR FILING DATE: 1999-10-01
 PRIOR APPLICATION NUMBER: 60/156,633
 PRIOR FILING DATE: 1999-09-29
 NUMBER OF SEQ ID NOS: 146
 SOFTWARE: PatentIn version 3.0
 SEQ ID NO 28
 LENGTH: 370
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-416-760-28

Query Match 100.0%; Score 1963; DB 18; Length 370;
 Best Local Similarity 100.0%; Pred. No. 4,6e-182;
 Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 1 MANYSHADNIIIONISPLAFKLTSLGFTIGSVYGNLLISILVYDKTLHAPYFELL 60
 1 MANTSHADNIIIONISPLAFKLTSLGFTIGSVYGNLLISILVYDKTLHAPYFELL 60

QY 61 DLCCSDILRSATCPPEVNSVKNSTWYGTLTCKVIAFLGVLSCFHTAFMFCISVTRY 120
 DB 61 DLCCSDILRSATCPPEVNSVKNSTWYGTLTCKVIAFLGVLSCFHTAFMFCISVTRY 120
 QY 121 LAIAHREYTRKLTFTWCLAVICWMTLSVMAAPPVLDVGTYSFIREDDCTFOHRSFR 180
 DB 121 LAIAHREYTRKLTFTWCLAVICWMTLSVMAAPPVLDVGTYSFIREDDCTFOHRSFR 180
 QY 181 ANDSLGFMILLALILATQVLYLKIIFVHDKKKPVQVAAVSQNMWTFHGPASGQA 240
 DB 181 ANDSLGFMILLALILATQVLYLKIIFVHDKKKPVQVAAVSQNMWTFHGPASGQA 240
 QY 241 ANWLAGEGRTPTLLIGIRONANTGRRLLVDEFEKMERISMFTIMFTLTLNGP 300
 DB 241 ANWLAGEGRTPTLLIGIRONANTGRRLLVDEFEKMERISMFTIMFTLTLNGP 300
 QY 301 YLVACYRVEFARGPVPGFLLTAVMNSFAQAGINPEFCISNRLRCFSTLLYCKRS 360
 DB 301 YLVACYRVEFARGPVPGFLLTAVMNSFAQAGINPEFCISNRLRCFSTLLYCKRS 360
 QY 361 RLPREPYCVI 370
 DB 361 RLPREPYCVI 370

RESULT 5
 US-09-416-760A-28
 Sequence 28, Application US/09416760A
 GENERAL INFORMATION:
 APPLICANT: Behan, Dominic P.
 APPLICANT: Lehmann-Brulisma, Karin
 APPLICANT: Chalmers, Derek T.
 APPLICANT: Lowitz, Kevin P.
 APPLICANT: Lin, I-Lin
 APPLICANT: Dang, Huong T.
 APPLICANT: Chen, Ruoping
 APPLICANT: Liaw, Chen W.
 TITLE OF INVENTION: Non-Endogenous Constitutively Activated Human G Protein Coupled
 FILE REFERENCE: AREN-0054
 CURRENT APPLICATION NUMBER: US/09/416,760A
 PRIOR FILING DATE: 1999-10-12
 PRIOR APPLICATION NUMBER: 09/170,496
 PRIOR FILING DATE: 1998-10-13
 PRIOR APPLICATION NUMBER: 60/110,060
 PRIOR FILING DATE: 1998-11-27
 PRIOR APPLICATION NUMBER: 60/120,416
 PRIOR FILING DATE: 1999-02-16
 PRIOR APPLICATION NUMBER: 60/121,852
 PRIOR FILING DATE: 1999-02-26
 PRIOR APPLICATION NUMBER: 60/109,213
 PRIOR FILING DATE: 1998-11-20
 PRIOR APPLICATION NUMBER: 60/123,944
 PRIOR FILING DATE: 1999-03-12
 PRIOR APPLICATION NUMBER: 60/123,945
 PRIOR FILING DATE: 1999-03-12
 PRIOR APPLICATION NUMBER: 60/123,948
 PRIOR FILING DATE: 1999-03-12
 PRIOR APPLICATION NUMBER: 60/123,951
 PRIOR FILING DATE: 1999-03-12
 PRIOR APPLICATION NUMBER: 60/123,946
 PRIOR FILING DATE: 1999-03-12
 PRIOR APPLICATION NUMBER: 60/123,949
 PRIOR FILING DATE: 1999-03-12
 PRIOR APPLICATION NUMBER: 60/152,524
 PRIOR FILING DATE: 1999-09-03
 PRIOR APPLICATION NUMBER: 60/151,114
 PRIOR FILING DATE: 1999-08-27
 PRIOR APPLICATION NUMBER: 60/108,029
 PRIOR FILING DATE: 1998-11-12
 PRIOR APPLICATION NUMBER: 60/136,436
 PRIOR FILING DATE: 1999-05-28
 PRIOR APPLICATION NUMBER: 60/136,439
 PRIOR FILING DATE: 1999-05-28

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PRIOR APPLICATION NUMBER: 60/136,567
PRIOR FILING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: 60/137,127
PRIOR FILING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: 60/137,131
PRIOR FILING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: 60/141,448
PRIOR FILING DATE: 1999-06-29
PRIOR APPLICATION NUMBER: 60/136,437
PRIOR FILING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: 60/156,555
PRIOR FILING DATE: 1999-09-29
PRIOR APPLICATION NUMBER: 60/156,634
PRIOR FILING DATE: 1999-09-29
PRIOR APPLICATION NUMBER: 60/157,280
PRIOR FILING DATE: 1999-10-01
PRIOR APPLICATION NUMBER: 60/157,294
PRIOR FILING DATE: 1999-10-01
PRIOR APPLICATION NUMBER: 60/157,281
PRIOR FILING DATE: 1999-10-01
PRIOR APPLICATION NUMBER: 60/157,282
PRIOR FILING DATE: 1999-10-01
PRIOR APPLICATION NUMBER: 60/156,633
PRIOR FILING DATE: 1999-09-29
NUMBER OF SEQ ID NOS: 149
SOFTWARE: PatentIn version 3.1
SEQ ID NO 28
LENGTH: 370
TYPE: PRT
ORGANISM: Homo sapiens
US-09-416-760A-28

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Query Match      100.0%; Score 1963; DB 18; Length 370;
Best Local Similarity 100.0%; Pred. No. 4,6e-182;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MANYSHADNIIQNLSPFLAFLKLTSLGFIIGSVVGNLLISILVYDKTLHRAPIYFLL 60
DB 1 MANYSHADNIIQNLSPFLAFLKLTSLGFIIGSVVGNLLISILVYDKTLHRAPIYFLL 60
QY 61 DCCSDILRSALICFPFVNSVKNKSTWYGTICKVIAFLGVLSCFHTAFMLFCISVTRY 120
DB 61 DCCSDILRSALICFPFVNSVKNKSTWYGTICKVIAFLGVLSCFHTAFMLFCISVTRY 120
QY 121 LAIAHHRFTYKRLTFWCLAVICWMTLSVMAFPVLDVGTSTFIREDOCTFOHRSFR 180
DB 121 LAIAHHRFTYKRLTFWCLAVICWMTLSVMAFPVLDVGTSTFIREDOCTFOHRSFR 180
QY 181 ANDSLGFMILLALITATOLVYKLIFFVHRRKMKPVQFVAASQNMWTFHGGASQAA 240
DB 181 ANDSLGFMILLALITATOLVYKLIFFVHRRKMKPVQFVAASQNMWTFHGGASQAA 240
QY 241 ANMLAGFGRPPTLLIGIRONANTTGRRLVLDEFKMKRISRMFYIMTFELTLMP 300
DB 241 ANMLAGFGRPPTLLIGIRONANTTGRRLVLDEFKMKRISRMFYIMTFELTLMP 300
QY 301 YIVACYWRFVARGPVVGGFELTAAMVMSFAQAGINPVCIFSNRELRCSTLLYCRKS 360
DB 301 YIVACYWRFVARGPVVGGFELTAAMVMSFAQAGINPVCIFSNRELRCSTLLYCRKS 360
QY 361 RLREPYCVI 370
DB 361 RLREPYCVI 370

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RESULT 6
US-09-417-044-26
Sequence 26, Application US/09417044
GENERAL INFORMATION:
APPLICANT: Chen, Ruoping

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APPLICANT: Dang, Huang T.
APPLICANT: Liaw, Chen W.
TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors
FILE REFERENCE: AREN0050
CURRENT APPLICATION NUMBER: US/09/417,044
Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 74
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 26
LENGTH: 370
TYPE: PRT
ORGANISM: Homo sapiens
US-09-417-044-26

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Query Match      100.0%; Score 1963; DB 18; Length 370;
Best Local Similarity 100.0%; Pred. No. 4,6e-182;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MANYSHADNIIQNLSPFLAFLKLTSLGFIIGSVVGNLLISILVYDKTLHRAPIYFLL 60
DB 1 MANYSHADNIIQNLSPFLAFLKLTSLGFIIGSVVGNLLISILVYDKTLHRAPIYFLL 60
QY 61 DCCSDILRSALICFPFVNSVKNKSTWYGTICKVIAFLGVLSCFHTAFMLFCISVTRY 120
DB 61 DCCSDILRSALICFPFVNSVKNKSTWYGTICKVIAFLGVLSCFHTAFMLFCISVTRY 120
QY 121 LAIAHHRFTYKRLTFWCLAVICWMTLSVMAFPVLDVGTSTFIREDOCTFOHRSFR 180
DB 121 LAIAHHRFTYKRLTFWCLAVICWMTLSVMAFPVLDVGTSTFIREDOCTFOHRSFR 180
QY 181 ANDSLGFMILLALITATOLVYKLIFFVHRRKMKPVQFVAASQNMWTFHGGASQAA 240
DB 181 ANDSLGFMILLALITATOLVYKLIFFVHRRKMKPVQFVAASQNMWTFHGGASQAA 240
QY 241 ANMLAGFGRPPTLLIGIRONANTTGRRLVLDEFKMKRISRMFYIMTFELTLMP 300
DB 241 ANMLAGFGRPPTLLIGIRONANTTGRRLVLDEFKMKRISRMFYIMTFELTLMP 300
QY 301 YIVACYWRFVARGPVVGGFELTAAMVMSFAQAGINPVCIFSNRELRCSTLLYCRKS 360
DB 301 YIVACYWRFVARGPVVGGFELTAAMVMSFAQAGINPVCIFSNRELRCSTLLYCRKS 360
QY 361 RLREPYCVI 370
DB 361 RLREPYCVI 370

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```

RESULT 7
US-09-427-653-2
Sequence 2, Application US/09427653A
GENERAL INFORMATION:
APPLICANT: Vogell, Gabriel
APPLICANT: Wood, Linda
TITLE OF INVENTION: G Protein-coupled Receptor CON202, Expressed in Brain
FILE REFERENCE: 28341/6264
CURRENT APPLICATION NUMBER: US/09/427,653A
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 370
TYPE: PRT
ORGANISM: Homo sapiens
US-09-427-653-2

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Query Match      100.0%; Score 1963; DB 18; Length 370;
Best Local Similarity 100.0%; Pred. No. 4,6e-182;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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US-09-622-439-24
Sequence 24, Application US/09622439
GENERAL INFORMATION:
APPLICANT: Yamanouchi Pharmaceutical Co., Ltd.
TITLE OF INVENTION: A novel G protein coupled receptor protein
FILE REFERENCE: 19905
CURRENT APPLICATION NUMBER: US/09/622,439
CURRENT FILING DATE: 2000-08-17
PRIOR APPLICATION NUMBER: JP P1998-060245
PRIOR FILING DATE: 1998-03-12
PRIOR APPLICATION NUMBER: JP P1999-026774
PRIOR FILING DATE: 1999-02-03
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentia Ver. 2.0
SEQ ID NO 24
LENGTH: 370
TYPE: PRT
ORGANISM: Rattus sp.
US-09-622-439-24

Query Match 100.0%; Score 1963; DB 20; Length 370;
Best Local Similarity 100.0%; Pred. No. 4,6e-182;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MANYSHADNIIQNTSLPTAFKLTSLGFIIGSVVGNLLISILVKDKTLHRAPIYFLL 60
DB 1 MANYSHADNIIQNTSLPTAFKLTSLGFIIGSVVGNLLISILVKDKTLHRAPIYFLL 60
QY 61 DICCSDLRSALCFPPFVNSVKNSTWTYGTLCCKVIAFLGVISCFHTAMLCISVTRY 120
DB 61 DICCSDLRSALCFPPFVNSVKNSTWTYGTLCCKVIAFLGVISCFHTAMLCISVTRY 120
QY 121 LAIAHREFTKRLTFMTCLAVICMWTLSVMAAFPPVLDVGTYSFIREDOCTFOHRSFR 180
DB 121 LAIAHREFTKRLTFMTCLAVICMWTLSVMAAFPPVLDVGTYSFIREDOCTFOHRSFR 180
QY 121 LAIAHREFTKRLTFMTCLAVICMWTLSVMAAFPPVLDVGTYSFIREDOCTFOHRSFR 180
DB 121 LAIAHREFTKRLTFMTCLAVICMWTLSVMAAFPPVLDVGTYSFIREDOCTFOHRSFR 180
QY 181 ANDSLGFMILLALILLATQLVYLKLIFFVHRRKMKPVQFAAVSONMTFHGPGASQAA 240
DB 181 ANDSLGFMILLALILLATQLVYLKLIFFVHRRKMKPVQFAAVSONMTFHGPGASQAA 240
QY 241 ANMLAGRGPTPTLLIGIQONANTTGRRLVLDDEKMKRISRMVYIMTFLETLTMRP 300
DB 241 ANMLAGRGPTPTLLIGIQONANTTGRRLVLDDEKMKRISRMVYIMTFLETLTMRP 300
QY 301 YIVACYRVARFARGVYVGGFLLTAAVMSPFOAGINPVCIFSNRELRCFSTTLTYCRKS 360
DB 301 YIVACYRVARFARGVYVGGFLLTAAVMSPFOAGINPVCIFSNRELRCFSTTLTYCRKS 360
QY 361 RLPREPYCVI 370
DB 361 RLPREPYCVI 370

RESULT 11
US-09-698-419-14
Sequence 14, Application US/09698419
GENERAL INFORMATION:
APPLICANT: Vogell, Gabriel
APPLICANT: Wood, Linda S.
APPLICANT: Merchant, Kalpana
TITLE OF INVENTION: G PROTEIN-COUPLED RECEPTORS EXPRESSED IN BRAIN
FILE REFERENCE: 28341/6276NCP
CURRENT APPLICATION NUMBER: US/09/698,419
CURRENT FILING DATE: 2000-10-27
PRIOR APPLICATION NUMBER: US 09/481,794
PRIOR FILING DATE: 2000-01-12
PRIOR APPLICATION NUMBER: US 09/454,399
PRIOR FILING DATE: 1999-12-03
PRIOR APPLICATION NUMBER: US 09/429,517
PRIOR FILING DATE: 1999-10-28
PRIOR APPLICATION NUMBER: US 09/429,555
PRIOR FILING DATE: 1999-10-28

PRIOR APPLICATION NUMBER: US 09/429,676
PRIOR FILING DATE: 1999-10-28
PRIOR APPLICATION NUMBER: US 09/429,695
PRIOR FILING DATE: 1999-10-28
PRIOR APPLICATION NUMBER: US 09/428,114
PRIOR FILING DATE: 1999-10-27
PRIOR APPLICATION NUMBER: US 09/428,020
PRIOR FILING DATE: 1999-10-27
PRIOR APPLICATION NUMBER: US 09/427,859
PRIOR FILING DATE: 1999-10-27
PRIOR APPLICATION NUMBER: US 09/427,653
PRIOR FILING DATE: 1999-10-27
NUMBER OF SEQ ID NOS: 75
SOFTWARE: Patentia Ver. 2.0
SEQ ID NO 14
LENGTH: 370
TYPE: PRT
ORGANISM: Homo sapiens
US-09-698-419-14

Query Match 100.0%; Score 1963; DB 20; Length 370;
Best Local Similarity 100.0%; Pred. No. 4,6e-182;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MANYSHADNIIQNTSLPTAFKLTSLGFIIGSVVGNLLISILVKDKTLHRAPIYFLL 60
DB 1 MANYSHADNIIQNTSLPTAFKLTSLGFIIGSVVGNLLISILVKDKTLHRAPIYFLL 60
QY 61 DICCSDLRSALCFPPFVNSVKNSTWTYGTLCCKVIAFLGVISCFHTAMLCISVTRY 120
DB 61 DICCSDLRSALCFPPFVNSVKNSTWTYGTLCCKVIAFLGVISCFHTAMLCISVTRY 120
QY 121 LAIAHREFTKRLTFMTCLAVICMWTLSVMAAFPPVLDVGTYSFIREDOCTFOHRSFR 180
DB 121 LAIAHREFTKRLTFMTCLAVICMWTLSVMAAFPPVLDVGTYSFIREDOCTFOHRSFR 180
QY 121 LAIAHREFTKRLTFMTCLAVICMWTLSVMAAFPPVLDVGTYSFIREDOCTFOHRSFR 180
DB 121 LAIAHREFTKRLTFMTCLAVICMWTLSVMAAFPPVLDVGTYSFIREDOCTFOHRSFR 180
QY 181 ANDSLGFMILLALILLATQLVYLKLIFFVHRRKMKPVQFAAVSONMTFHGPGASQAA 240
DB 181 ANDSLGFMILLALILLATQLVYLKLIFFVHRRKMKPVQFAAVSONMTFHGPGASQAA 240
QY 241 ANMLAGRGPTPTLLIGIQONANTTGRRLVLDDEKMKRISRMVYIMTFLETLTMRP 300
DB 241 ANMLAGRGPTPTLLIGIQONANTTGRRLVLDDEKMKRISRMVYIMTFLETLTMRP 300
QY 301 YIVACYRVARFARGVYVGGFLLTAAVMSPFOAGINPVCIFSNRELRCFSTTLTYCRKS 360
DB 301 YIVACYRVARFARGVYVGGFLLTAAVMSPFOAGINPVCIFSNRELRCFSTTLTYCRKS 360
QY 361 RLPREPYCVI 370
DB 361 RLPREPYCVI 370

RESULT 12
US-09-875-076-26
Sequence 26, Application US/09875076
GENERAL INFORMATION:
APPLICANT: Chen, Ruoping
APPLICANT: Dang, Huong T.
APPLICANT: Liaw, Chen W.
APPLICANT: Lin, I-Lin
TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors
FILE REFERENCE: AREN0050
CURRENT APPLICATION NUMBER: US/09/875,076
CURRENT FILING DATE: 2001-06-06
PRIOR APPLICATION NUMBER: 09/417,044
PRIOR FILING DATE: 1999-10-12
PRIOR APPLICATION NUMBER: 60/120,416
PRIOR FILING DATE: 1999-02-16
PRIOR APPLICATION NUMBER: 60/121,851
PRIOR FILING DATE: 1999-02-26
PRIOR APPLICATION NUMBER: 60/123,946

PRIOR FILING DATE: 1999-03-12
PRIOR APPLICATION NUMBER: 60/123,949
PRIOR FILING DATE: 1999-03-12
PRIOR APPLICATION NUMBER: 60/136,436
PRIOR FILING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: 60/136,437
PRIOR FILING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: 60/136,439
PRIOR FILING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: 60/136,567
PRIOR FILING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: 60/137,127
PRIOR FILING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: 60/137,131
PRIOR FILING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: 60/141,448
PRIOR FILING DATE: 1999-06-29
PRIOR APPLICATION NUMBER: 60/156,653
PRIOR FILING DATE: 1999-09-29
PRIOR APPLICATION NUMBER: 60/156,633
PRIOR FILING DATE: 1999-09-29
PRIOR APPLICATION NUMBER: 60/156,555
PRIOR FILING DATE: 1999-09-29
PRIOR APPLICATION NUMBER: 60/156,634
PRIOR FILING DATE: 1999-09-29
PRIOR APPLICATION NUMBER: 60/157,280
PRIOR FILING DATE: 1999-10-01
PRIOR APPLICATION NUMBER: 60/157,294
PRIOR FILING DATE: 1999-10-01
PRIOR APPLICATION NUMBER: 60/157,281
PRIOR FILING DATE: 1999-10-01
PRIOR APPLICATION NUMBER: 60/157,293
PRIOR FILING DATE: 1999-10-01
PRIOR APPLICATION NUMBER: 60/157,282
PRIOR FILING DATE: 1999-10-01
NUMBER OF SEQ ID NOS: 74
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 26
LENGTH: 370
TYPE: PRT
ORGANISM: Homo sapiens
US-09-875-076-26

Query Match 100.0%; Score 1963; DB 22; Length 370;
Best Local Similarity 100.0%; Pred. No. 4.6e-182;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MANYSHADNITQNSPLTAFKLSLGIIVSVYGNLLISILVKKDTLHAPYFLL 60
DB 1 MANSHADNITQNSPLTAFKLSLGIIVSVYGNLLISILVKKDTLHAPYFLL 60
QY 61 DLCCSDILRSALCFPEFVNSVKNSTWYGTCTCKVIAFLGVLSCHPTAFMELCISVTRY 120
DB 61 DLCCSDILRSALCFPEFVNSVKNSTWYGTCTCKVIAFLGVLSCHPTAFMELCISVTRY 120
QY 121 LAIAHREYTRKLTFTWCTAVICNWTLSVANAAPPVLDVGYSTFREDDQCFQHRSR 180
DB 121 LAIAHREYTRKLTFTWCTAVICNWTLSVANAAPPVLDVGYSTFREDDQCFQHRSR 180
QY 181 ANDSGFMILLALLILLOLVYLKLIFFVHDKRKKPVQVFAVAVSONMTFHHGASGQAA 240
DB 181 ANDSGFMILLALLILLOLVYLKLIFFVHDKRKKPVQVFAVAVSONMTFHHGASGQAA 240
QY 241 ANNLAGEFGPPTPLIGIRONANTGRRRLVLDDEKKEKRISRMFYTMTEFLTLMP 300
DB 241 ANNLAGEFGPPTPLIGIRONANTGRRRLVLDDEKKEKRISRMFYTMTEFLTLMP 300
QY 301 YLVACYWVEFARGPVPGGFLTAAVMSFAQGINPEVCIFSNRELRLRCFSTLLYCRS 360
DB 301 YLVACYWVEFARGPVPGGFLTAAVMSFAQGINPEVCIFSNRELRLRCFSTLLYCRS 360
QY 361 RLREPYCVI 370

DB 361 RLREPYCVI 370
RESULT 13
US-09-876-252-28
Sequence 28, Application US/09876252
GENERAL INFORMATION:
APPLICANT: Behan, Dominic P.
APPLICANT: Lehmann-Brulsma, Karin
APPLICANT: Chalmers, Derek T.
APPLICANT: Lowitz, Kevin P.
APPLICANT: Lin, I-Lin
APPLICANT: Dang, Huong T.
APPLICANT: Chen, Ruoping
TITLE OF INVENTION: Non-Endogenous Constitutively Activated Human G Protein Coupled
FILE REFERENCE: AREN-0054
CURRENT APPLICATION NUMBER: US/09/876,252
PRIOR FILING DATE: 2001-06-07
PRIOR APPLICATION NUMBER: 09/416,760
PRIOR FILING DATE: 1999-10-12
PRIOR APPLICATION NUMBER: 09/170,496
PRIOR FILING DATE: 1998-10-13
PRIOR APPLICATION NUMBER: 60/110,060
PRIOR FILING DATE: 1998-11-27
PRIOR APPLICATION NUMBER: 60/120,416
PRIOR FILING DATE: 1999-02-16
PRIOR APPLICATION NUMBER: 60/121,852
PRIOR FILING DATE: 1999-02-26
PRIOR APPLICATION NUMBER: 60/109,213
PRIOR FILING DATE: 1998-11-20
PRIOR APPLICATION NUMBER: 60/123,944
PRIOR FILING DATE: 1999-03-12
PRIOR APPLICATION NUMBER: 60/123,945
PRIOR FILING DATE: 1999-03-12
PRIOR APPLICATION NUMBER: 60/123,948
PRIOR FILING DATE: 1999-03-12
PRIOR APPLICATION NUMBER: 60/123,951
PRIOR FILING DATE: 1999-03-12
PRIOR APPLICATION NUMBER: 60/123,946
PRIOR FILING DATE: 1999-03-12
PRIOR APPLICATION NUMBER: 60/123,949
PRIOR FILING DATE: 1999-03-12
PRIOR APPLICATION NUMBER: 60/152,524
PRIOR FILING DATE: 1999-09-03
PRIOR APPLICATION NUMBER: 60/151,114
PRIOR FILING DATE: 1999-08-27
PRIOR APPLICATION NUMBER: 60/108,029
PRIOR FILING DATE: 1998-11-12
PRIOR APPLICATION NUMBER: 60/136,436
PRIOR FILING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: 60/136,439
PRIOR FILING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: 60/136,567
PRIOR FILING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: 60/137,127
PRIOR FILING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: 60/137,131
PRIOR FILING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: 60/141,448
PRIOR FILING DATE: 1999-06-29
PRIOR APPLICATION NUMBER: 60/136,437
PRIOR FILING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: 60/156,555
PRIOR FILING DATE: 1999-09-29
PRIOR APPLICATION NUMBER: 60/156,634
PRIOR FILING DATE: 1999-09-29
PRIOR APPLICATION NUMBER: 60/156,653
PRIOR FILING DATE: 1999-09-29
PRIOR APPLICATION NUMBER: 60/157,280
PRIOR FILING DATE: 1999-10-01
PRIOR APPLICATION NUMBER: 60/157,294

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PRIOR FILING DATE: 1999-10-01
PRIOR APPLICATION NUMBER: 60/157,281
PRIOR FILING DATE: 1999-10-01
PRIOR APPLICATION NUMBER: 60/157,282
PRIOR FILING DATE: 1999-10-01
PRIOR APPLICATION NUMBER: 60/156,633
PRIOR FILING DATE: 1999-09-29
NUMBER OF SEQ ID NOS: 146
SOFTWARE: PatentIn version 3.0
SEQ ID NO 28
LENGTH: 370
TYPE: PRT
ORGANISM: Homo sapiens
US-09-876-252-28

Query Match      100.0%; Score 1963; DB 22; Length 370;
Best Local Similarity 100.0%; Pred. No. 4.6e-182;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MANTSHADNIIQNLSPITAFKLTSLGFIIGSVVGNLLISILVKKDKTLHRAPIYFLL 60
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QY 61 DLCCSDILRSALICFPFVNSVKNKSTWYGTITCKVIAFLGVLSCFHTAFMLFCISVTRY 120
    |||||||
DB 61 DLCCSDILRSALICFPFVNSVKNKSTWYGTITCKVIAFLGVLSCFHTAFMLFCISVTRY 120
    |||||||

QY 121 LAIAHHRFTKRLTFWTCIAVICMWTLSVAMAFPPVLDVGTYSFIREDOCTFOHRSFR 180
    |||||||
DB 121 LAIAHHRFTKRLTFWTCIAVICMWTLSVAMAFPPVLDVGTYSFIREDOCTFOHRSFR 180
    |||||||

QY 181 ANDSLGFMILLALILATOLVYLKLIFFVHDRKKMPVOEFAVAVSONMTFHGASGQAA 240
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DB 181 ANDSLGFMILLALILATOLVYLKLIFFVHDRKKMPVOEFAVAVSONMTFHGASGQAA 240
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QY 241 ANMLAGFGRPPTLLGIRONANTTGRRLVLVDEFKMEKRSIRMEYIMTFLETLTLMGP 300
    |||||||
DB 241 ANMLAGFGRPPTLLGIRONANTTGRRLVLVDEFKMEKRSIRMEYIMTFLETLTLMGP 300
    |||||||

QY 301 YIVACYWRFARGPVYPGGFLTAAVMMSFAQAGINPVCIFSNRELRCFSTLLYCRKS 360
    |||||||
DB 301 YIVACYWRFARGPVYPGGFLTAAVMMSFAQAGINPVCIFSNRELRCFSTLLYCRKS 360
    |||||||

QY 361 RLPREPYCVI 370
    |||||||
DB 361 RLPREPYCVI 370
    |||||||

RESULT 14
US-09-988-922-16
Sequence 16, Application US/09988922
GENERAL INFORMATION:
APPLICANT: Erding Hu
APPLICANT: Yuan Zhu
APPLICANT: Ganesh M. Sathe
APPLICANT: Joyce Yue Mao
APPLICANT: Wendy S. Halsey
APPLICANT: Jon Chambers
APPLICANT: Allison Isobel Muir
APPLICANT: Phillip Graham Szekeres
APPLICANT: Derek J. Bergsma
APPLICANT: Usman Shadon
APPLICANT: Nabil A. Elshourbagy
APPLICANT: David Michalovich
APPLICANT: Pamela A. Lane
APPLICANT: Menelas N. Pangalos
APPLICANT: Melanie Robbins
APPLICANT: David Malcolm Duckworth
APPLICANT: Jeffrey Hill
APPLICANT: Ping Tsui
APPLICANT: Pankaj Agarwal
APPLICANT: Randall Forrest Smith
```

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APPLICANT: Lisa Vawter
APPLICANT: Catherine E. Ellis
APPLICANT: Mahanandeeswar Gattu
APPLICANT: John W. Quillen, Jr.
APPLICANT: Erin M. Toland
APPLICANT: Steven Michael Foord
APPLICANT: Han Ngoc Trinh
APPLICANT: Alexander Taylor
APPLICANT: Henry Sarau
APPLICANT: Steven Ruben
APPLICANT: George H. Poste
APPLICANT: Michel Louis Souchet
APPLICANT: Philippe Laurent Robert
APPLICANT: Stephane Clement Krief
APPLICANT: Bernard Emile Joseph Gout
APPLICANT: Eve Mahe
TITLE OF INVENTION: HUMAN G PROTEIN-COUPLED RECEPTOR
TITLE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES
FILE REFERENCE: GP-70775B-C1
CURRENT FILING DATE: 2001-11-19
NUMBER OF SEQ ID NOS: 82
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 16
LENGTH: 370
TYPE: PRT
ORGANISM: HOMO SAPIENS
US-09-988-922-16

Query Match      100.0%; Score 1963; DB 23; Length 370;
Best Local Similarity 100.0%; Pred. No. 4.6e-182;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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    |||||||
DB 1 MANTSHADNIIQNLSPITAFKLTSLGFIIGSVVGNLLISILVKKDKTLHRAPIYFLL 60
    |||||||

QY 61 DLCCSDILRSALICFPFVNSVKNKSTWYGTITCKVIAFLGVLSCFHTAFMLFCISVTRY 120
    |||||||
DB 61 DLCCSDILRSALICFPFVNSVKNKSTWYGTITCKVIAFLGVLSCFHTAFMLFCISVTRY 120
    |||||||

QY 121 LAIAHHRFTKRLTFWTCIAVICMWTLSVAMAFPPVLDVGTYSFIREDOCTFOHRSFR 180
    |||||||
DB 121 LAIAHHRFTKRLTFWTCIAVICMWTLSVAMAFPPVLDVGTYSFIREDOCTFOHRSFR 180
    |||||||

QY 181 ANDSLGFMILLALILATOLVYLKLIFFVHDRKKMPVOEFAVAVSONMTFHGASGQAA 240
    |||||||
DB 181 ANDSLGFMILLALILATOLVYLKLIFFVHDRKKMPVOEFAVAVSONMTFHGASGQAA 240
    |||||||

QY 241 ANMLAGFGRPPTLLGIRONANTTGRRLVLVDEFKMEKRSIRMEYIMTFLETLTLMGP 300
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DB 241 ANMLAGFGRPPTLLGIRONANTTGRRLVLVDEFKMEKRSIRMEYIMTFLETLTLMGP 300
    |||||||

QY 301 YIVACYWRFARGPVYPGGFLTAAVMMSFAQAGINPVCIFSNRELRCFSTLLYCRKS 360
    |||||||
DB 301 YIVACYWRFARGPVYPGGFLTAAVMMSFAQAGINPVCIFSNRELRCFSTLLYCRKS 360
    |||||||

QY 361 RLPREPYCVI 370
    |||||||
DB 361 RLPREPYCVI 370
    |||||||

RESULT 15
US-10-043-945-2
Sequence 2, Application US/10043945
GENERAL INFORMATION:
APPLICANT: Smith, Kelli E.
APPLICANT: Pathirana, Marie Sudam
APPLICANT: Kyaw, Hla
APPLICANT: Borowsky, Beth E.
TITLE OF INVENTION: DNA ENCODING ORPHAN SNORF12 RECEPTOR
FILE REFERENCE: 58801
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: CURRENT APPLICATION NUMBER: US/10/043,945
 : CURRENT FILING DATE: 2002-01-10
 : PRIOR APPLICATION NUMBER: 09/264,041
 : NUMBER OF SEQ ID NOS: 2
 : SOFTWARE: PatentIn Ver. 2.0 - beta
 : SEQ ID NO 2
 : LENGTH: 370
 : TYPE: PRT
 : ORGANISM: Homo sapiens
 : US-10-043-945-2

Query Match 100.0% Score 1963; DB 24; Length 370;
 Best Local Similarity 100.0%; Pred. No. 4.6e-182;
 Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db	1	MANYSHADNIIQNLSPITAFKLTSLGFLIGSVVGNLLISILVYKDKTLHRAPYYELL	60
QY	61	DIICSDILRSALICPFVENSVMKNGSTWYGTLCVKYIAFLGVLSCEHTAFMFCISVTRY	120
Db	61	DIICSDILRSALICPFVENSVMKNGSTWYGTLCVKYIAFLGVLSCEHTAFMFCISVTRY	120
QY	121	LAIAHREYTKRLTFWTCCLAVICMWTLSVMAFPVLDVGTYSFTREDOCTFOHRSFR	180
Db	121	LAIAHREYTKRLTFWTCCLAVICMWTLSVMAFPVLDVGTYSFTREDOCTFOHRSFR	180
QY	181	ANDSIGFMULLLILATOLVYLKLIFFVHDKKMKPVQFAVAVSONWTFHGPASGOAA	240
Db	181	ANDSIGFMULLLILATOLVYLKLIFFVHDKKMKPVQFAVAVSONWTFHGPASGOAA	240
QY	241	ANMLAGFGGPTPTLLGIRONANTGRRRLVLDFFKMEKRISRMFYIMTFLETLWGP	300
Db	241	ANMLAGFGGPTPTLLGIRONANTGRRRLVLDFFKMEKRISRMFYIMTFLETLWGP	300
QY	301	YIVACYWRYEARGPVVPGGFLTAAYVMSFAQAGINPFVCLFSNRELRCESTLLYCRKS	360
Db	301	YIVACYWRYEARGPVVPGGFLTAAYVMSFAQAGINPFVCLFSNRELRCESTLLYCRKS	360
QY	361	RLPREPYCVI 370	
Db	361	RLPREPYCVI 370	

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 Job time: 226 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 19, 2002, 14:38:24 ; Search time 21.56 seconds

(without alignments)
2133.035 Million cell updates/sec

Title: US-09-698-419-14

Perfect score: 1963
Sequence: 1 MANSYSHADNLTQNLSPFLTA.....STLLXCKRNPRLPYCVI 370

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 378952 seqs, 124292526 residues

Total number of hits satisfying chosen parameters: 378952

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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7: /cgn2_6/prodata/2/paa/US60_NEW_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1963	100.0	370	US-10-110-668-14	Sequence 14, App1
2	1963	100.0	370	US-10-125-749-16	Sequence 16, App1
3	1963	100.0	370	US-10-165-844-7	Sequence 7, App1
4	633	32.2	183	US-10-103-313-389	Sequence 389, App
5	577	29.4	144	US-10-103-313-394	Sequence 394, App
6	473	24.1	180	US-10-103-313-379	Sequence 379, App
7	470	23.9	143	US-10-130-469-62	Sequence 62, App1
8	337.5	17.2	106	US-10-130-469-30	Sequence 30, App1
9	264.5	13.5	478	US-10-176-255-31	Sequence 31, App1
10	258	13.1	470	US-10-176-255-25	Sequence 25, App1
11	257.5	13.1	453	US-10-127-940-7	Sequence 7, App1
12	256.5	13.1	478	US-10-176-255-33	Sequence 33, App1
13	253.5	12.9	470	US-10-166-101-8	Sequence 8, App1
14	253	12.9	448	US-10-127-940-3	Sequence 3, App1
15	252.5	12.9	470	US-60-380-336-52	Sequence 52, App1
16	247.5	12.6	447	US-10-157-031-10	Sequence 10, App1
17	243.5	12.4	388	US-10-157-031-123	Sequence 123, App
18	243.5	12.4	388	US-10-157-031-124	Sequence 124, App
19	241.5	12.3	460	US-10-166-101-4	Sequence 4, App1
20	241	12.3	458	US-10-176-255-27	Sequence 27, App1
21	239	12.2	422	US-10-118-804-13	Sequence 13, App1
22	239	12.2	422	US-10-166-101-3	Sequence 3, App1
23	237.5	12.1	497	US-10-127-940-2	Sequence 2, App1
24	237.5	12.1	497	US-09-568-255-2	Sequence 2, App1
25	237.5	12.1	497	US-10-052-589-2	Sequence 2, App1
26	237.5	12.1	515	US-10-130-461-11	Sequence 11, App1

27	237	12.1	458	6	US-10-176-255-29	Sequence 29, App1
28	235.5	12.0	453	6	US-10-127-940-4	Sequence 4, App1
29	233.5	11.9	402	1	PCT-US02-09785-750	Sequence 750, App
30	233.5	11.9	402	6	US-10-165-844-10	Sequence 10, App1
31	233.5	11.9	461	7	US-60-389-987-371	Sequence 371, App
32	233.5	11.9	466	6	US-09-952-680A-26	Sequence 26, App1
33	233.5	11.9	466	6	US-10-002-945-129	Sequence 129, App
34	232	11.8	565	6	US-10-130-461-12	Sequence 12, App1
35	230	11.7	428	6	US-10-127-940-5	Sequence 5, App1
36	229.5	11.7	501	7	US-60-360-039-7013	Sequence 7013, Ap
37	228.5	11.6	443	6	US-10-127-940-6	Sequence 6, App1
38	227.5	11.6	466	6	US-10-130-461-10	Sequence 10, App1
39	227.5	11.6	466	6	US-60-380-336-47	Sequence 47, App1
40	227	11.6	365	6	US-10-125-749-28	Sequence 28, App1
41	227	11.6	445	6	US-10-118-804-2	Sequence 2, App1
42	226.5	11.5	346	4	US-08-899-112B-30	Sequence 30, App1
43	224	11.4	387	4	US-08-899-112B-28	Sequence 28, App1
44	224	11.4	387	7	US-60-391-385-6	Sequence 6, App1
45	222	11.3	443	6	US-10-157-031-78	Sequence 78, App1

ALIGNMENTS

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RESULT 1
US-10-110-668-14
Sequence 14, Application US/10110668
GENERAL INFORMATION:
APPLICANT: Pharmacia & Upjohn Company
TITLE OR INVENTION: G PROTEIN-COUPLED RECEPTORS EXPRESSED IN BRAIN
FILE REFERENCE: 28341/6276P
CURRENT APPLICATION NUMBER: US/10/110, 668
CURRENT FILING DATE: 2002-04-15
PRIOR APPLICATION NUMBER: US 09/481,794
PRIOR FILING DATE: 2000-01-12
PRIOR APPLICATION NUMBER: US 09/454,399
PRIOR FILING DATE: 1999-12-03
PRIOR APPLICATION NUMBER: US 09/429,517
PRIOR FILING DATE: 1999-10-28
PRIOR APPLICATION NUMBER: US 09/429,555
PRIOR FILING DATE: 1999-10-28
PRIOR APPLICATION NUMBER: US 09/429,676
PRIOR FILING DATE: 1999-10-28
PRIOR APPLICATION NUMBER: US 09/429,695
PRIOR FILING DATE: 1999-10-28
PRIOR APPLICATION NUMBER: US 09/428,114
PRIOR FILING DATE: 1999-10-27
PRIOR APPLICATION NUMBER: US 09/428,020
PRIOR FILING DATE: 1999-10-27
PRIOR APPLICATION NUMBER: US 09/427,859
PRIOR FILING DATE: 1999-10-27
PRIOR APPLICATION NUMBER: US 09/427,653
PRIOR FILING DATE: 1999-10-27
NUMBER OF SEQ ID NOS: 75
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 14
LENGTH: 370
TYPE: PRT
ORGANISM: Homo sapiens
US-10-110-668-14

Query Match 100.0%; Score 1963; DB 6; Length 370;
Best Local Similarity 100.0%; Pred. No. 3 4e-168;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 MANSYSHADNLTQNLSPFLTA.....STLLXCKRNPRLPYCVI 60
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DB 61 DLCCSDILRSALICPPFVNSYKNGSTWYTGCTCKVIAFLVLSCFHRAFMFCISVRY 120

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OY 121 LAIAHRRYTKRLFTWTCIAVICMWTLSVAMAFPPVLDVGYTSFIREDOCTFOHRSFR 180
DB 121 LAIAHRRYTKRLFTWTCIAVICMWTLSVAMAFPPVLDVGYTSFIREDOCTFOHRSFR 180
OY 181 ANDSLGFMILLALITLALQOLVYLKLIFFVHDRKMKPVQFVAASQNMTHFGASGQAA 240
DB 181 ANDSLGFMILLALITLALQOLVYLKLIFFVHDRKMKPVQFVAASQNMTHFGASGQAA 240
OY 241 ANMLAGFGRGPTPTLLGIRONANTGRRRLVLDEFKMKRISRMFYIMTFLEFLTMGP 300
DB 241 ANMLAGFGRGPTPTLLGIRONANTGRRRLVLDEFKMKRISRMFYIMTFLEFLTMGP 300
OY 301 YLVACYWRVFARGPVPGGFLTAAVWMSFAQAGINPFVCIFSNRELRCFSTLLYCRKS 360
DB 301 YLVACYWRVFARGPVPGGFLTAAVWMSFAQAGINPFVCIFSNRELRCFSTLLYCRKS 360
OY 361 RLREPYCVI 370
DB 361 RLREPYCVI 370

RESULT 2
US-10-125-749-16
Sequence 16, Application US/10125749
GENERAL INFORMATION:
APPLICANT: Erding Hu
APPLICANT: Yuan Zhu
APPLICANT: Ganesh M. Sathe
APPLICANT: Joyce Yue Mao
APPLICANT: Wendy S. Halsey
APPLICANT: Jon Chambers
APPLICANT: Allison Isobel Muir
APPLICANT: Philip Graham Szekeres
APPLICANT: Usman Shabon
APPLICANT: Derek J. Bergsma
APPLICANT: Nabil A. Elshourbagy
APPLICANT: David Michalovich
APPLICANT: Pamela A. Lane
APPLICANT: Menelas N. Pangalos
APPLICANT: Melanie Robbins
APPLICANT: David Malcolm Duckworth
APPLICANT: Jeffrey Hill
APPLICANT: Ping Tsui
APPLICANT: Pankaj Agarwal
APPLICANT: Randall Forrest Smith
APPLICANT: Lisa Vawter
APPLICANT: Catherine E. Ellis
APPLICANT: Manhanandeeswar Gattu
APPLICANT: John W. Quillen, Jr.
APPLICANT: Erin M. Toland
APPLICANT: Steven Michael Foord
APPLICANT: Han Ngoc Triph
APPLICANT: Alexander Taylor
APPLICANT: Henry Sarau
APPLICANT: Steven Ruben
APPLICANT: George H. Postle
APPLICANT: Michel Louis Souchet
APPLICANT: Philippe Laurent Robert
APPLICANT: Stephane Clement Krief
APPLICANT: Bernard Emile Joseph Gout
APPLICANT: Eve Mahe
TITLE OF INVENTION: HUMAN G PROTEIN-COUPLED RECEPTOR
TITLE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES
FILE REFERENCE: GP-707758-C1
CURRENT FILING DATE: 2002-04-18
CURRENT FILING DATE: 2002-04-18
PRIOR FILING DATE: 2001-11-19
NUMBER OF SEQ ID NOS: 82
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 16
LENGTH: 370

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TYPE: PRI
ORGANISM: HOMO SAPIENS
US-10-125-749-16

Query Match 100.0%; Score 1963; DB 6; Length 370;
Best Local Similarity 100.0%; Pred. No. 3,4e-168;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 61 DLCCSDILRSALCFPEVENSVKNGSTWYGTLLCKVIAFLGVLSCFTAPMLFCISYTRY 120
OY 121 LAIAHRRYTKRLFTWTCIAVICMWTLSVAMAFPPVLDVGYTSFIREDOCTFOHRSFR 180
DB 121 LAIAHRRYTKRLFTWTCIAVICMWTLSVAMAFPPVLDVGYTSFIREDOCTFOHRSFR 180
OY 181 ANDSLGFMILLALITLALQOLVYLKLIFFVHDRKMKPVQFVAASQNMTHFGASGQAA 240
DB 181 ANDSLGFMILLALITLALQOLVYLKLIFFVHDRKMKPVQFVAASQNMTHFGASGQAA 240
OY 241 ANMLAGFGRGPTPTLLGIRONANTGRRRLVLDEFKMKRISRMFYIMTFLEFLTMGP 300
DB 241 ANMLAGFGRGPTPTLLGIRONANTGRRRLVLDEFKMKRISRMFYIMTFLEFLTMGP 300
OY 301 YLVACYWRVFARGPVPGGFLTAAVWMSFAQAGINPFVCIFSNRELRCFSTLLYCRKS 360
DB 301 YLVACYWRVFARGPVPGGFLTAAVWMSFAQAGINPFVCIFSNRELRCFSTLLYCRKS 360
OY 361 RLREPYCVI 370
DB 361 RLREPYCVI 370

RESULT 3
US-10-165-844-7
Sequence 7, Application US/10165844
GENERAL INFORMATION:
APPLICANT: Glucksman, Maria Alexandra
APPLICANT: Hodge, Martin R.
APPLICANT: Hunter, John J.
APPLICANT: Rudolph-Owen, Laura
APPLICANT: Welch, Nadine S.
TITLE OF INVENTION: Silos-Santlago, Immaculada
TITLE OF INVENTION: Novel Nucleic Acid Sequences Encoding
FILE REFERENCE: 35800/248302
CURRENT FILING DATE: 2002-06-07
CURRENT FILING DATE: 2002-06-07
PRIOR APPLICATION NUMBER: US 09/088,857
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: US 09/324,465
PRIOR FILING DATE: 1999-06-02
PRIOR APPLICATION NUMBER: US 09/464,685
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: US 09/741,783
PRIOR FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: US 09/145,745
PRIOR FILING DATE: 1998-09-02
PRIOR APPLICATION NUMBER: US 09/383,745
PRIOR FILING DATE: 1999-08-26
PRIOR APPLICATION NUMBER: US 09/234,923
PRIOR FILING DATE: 1999-01-21
PRIOR APPLICATION NUMBER: US 09/340,880
PRIOR FILING DATE: 1999-06-28
NUMBER OF SEQ ID NOS: 26
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 7
LENGTH: 370

```

```

; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-165-844-7

```

Query Match	100.0%;	Score 1963;	DB 6;	Length 370;
Best Local Similarity	100.0%;	Pred. No. 3.4e-168;		
Matches 370; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0;

[illegible]

```

RESULT      4
US-10-103-389
: Sequence 389: Application US/10103313
: GENERAL INFORMATION:
: APPLICANT: Rosen et al.
: TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
: FILE REFERENCE: P1207C1
: CURRENT APPLICATION NUMBER: US/10/103,313
: CURRENT FILING DATE: 2002-03-12
: NUMBER OF SEQ. ID NOS: 653
: Prior Application removed - See File Wrapper or Palm
SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 389
: LENGTH: 183
: TYPE: PRT
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (170)
: OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
: US-10-103-313-389

```

Query Match	32.2%	Score 633;	DB 6;	Length 183;
Best Local Similarity	62.9%	Pred. NO. 2.9e+49;		
Matches 112;	Conservative 31;	Mismatches 33;	Indels 2;	Gaps 1;

[illegible]

QY 119 RYLALAHHRFYKRLTEWTCCLAVICMWTLSVMAAFPPYLDVGYSFIREEDCTFOH 176
|:|||||. |: | | | | | | | | | | | | | | | | : |
Db 126 RYMALAHHRFYAKRMTLWTCALVICAMWTLVSMAAFPYPFDVGTXKFIREDCIFEH 183

```

RESULT      5
US-10-103-313-394
: Sequence 394: Application US/10103313
GENERAL INFORMATION:
APPLICANT: Rosen et al.
FILE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: P1207/1
CURRENT APPLICATION NUMBER: US/10/103,313
CURRENT FILING DATE: 2002-03-12
NUMBER OF SEQ ID NOS: 653
: Prior Application removed - See File Wrapper or Palm
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 394
LENGTH: 144
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (82)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: misc_feature
LOCATION: (86)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: misc_feature
LOCATION: (87)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: misc_feature
LOCATION: (106)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: misc_feature
LOCATION: (111)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: misc_feature
LOCATION: (113)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: misc_feature
LOCATION: (114)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: misc_feature
LOCATION: (125)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: misc_feature
LOCATION: (142)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-103-313-394

```

Query Match	29.48;	Score 577;	DB 6;	Length 144;
Best Local Similarity	93.48;	Pred. No. 2.4e-44;		
Matches 113; Conservative	0;	Mismatches 8;	Indels 0;	Gaps 0

QY	1	MANSHADNLOMLSPLEAFKLTSGFTIGVSVGNLLSILVMDKTLHRAPIYELL	60
	10	MANSHADNLOMLSPLEAFKLTSGFTIGVSVGNLLSILVMDKTLHRAPIYELL	69
QY	61	DLCSDILRSALCPFEVSNKNGSTWYGTILCKVAIEFGVLSCFHTAAMLICISVTRY	120
	70	DLCSDILRSALCPFEVSNKNGSTWYGTILCKVAIEFGVLXHXFTAPMELCIXTRY	129
QY	121	L 121	
Db	130	L 130	

RESULT 6
US-10-103-313-379
; Sequence 379, Application US/10103313
; GENERAL INFORMATION:

APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: P0207C1
CURRENT APPLICATION NUMBER: US/10/103,313
CURRENT FILING DATE: 2002-03-12
NUMBER OF SEQ ID NOS: 653
Prior Application removed - See File Wrapper or Palm
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 379
LENGTH: 180
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (146)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: misc_feature
LOCATION: (152)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: misc_feature
LOCATION: (164)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: misc_feature
LOCATION: (171)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: misc_feature
LOCATION: (175)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-103-313-379

Query Match 24.1%; Score 473; DB 6; Length 180;
Best Local Similarity 52.4%; Pred. No. 6, 3e-35;
Matches 86; Conservative 33; Mismatches 37; Indels 8; Gaps 3;

QY 1 MANTSHADNIIQNTSP--LTAFKLTSLGFIIGSVGNLISILVCKDTHRAPYF 58
DB 6 MANTGEPEEVSGALSPSASATYKLVLTGLIMCVSLAGNALISLVKRALHRAKYF 65
QY 59 LLDCCSDILRSALICFPFVNSVKNSTWTYGLTCKVIAFLGVLSCEFTAFMLFCISVT 118
DB 66 LLDCLADGIRSAVCFPPVYASVRHGSSWTFSAISCKIVAFMAVLCFHFAPMLFCISVT 125
QY 119 RYLAIAHHRFYTKRLTFWTCLAVT-----CM-VWTLVSMAFPP 156
DB 126 RYMAIAHHRFYAKRMTLMTWCXAASAMXGCLPMPFHLTLTWAP 169

RESULT 7
US-10-130-469-62
Sequence 62, Application US/10130469
GENERAL INFORMATION:
APPLICANT: Vogell, Gabriel
APPLICANT: Huff, Rita
APPLICANT: Sejlitz, Torsten
APPLICANT: Lind, Peter
APPLICANT: Slightom, Jerry
APPLICANT: Schellin, Kathleen
APPLICANT: Bannigan, Chris
APPLICANT: Ruff, Valerie
APPLICANT: Kayles, Paul
APPLICANT: Wood, Linda
APPLICANT: Parodi, Luis
APPLICANT: Hiesch, Ronald
TITLE OF INVENTION: Novel G Protein Coupled Receptors
FILE REFERENCE: 237.PIUS
CURRENT APPLICATION NUMBER: US/10/130,469
PRIOR FILING DATE: 2002-05-16
PRIOR APPLICATION NUMBER: 60/165,838
PRIOR FILING DATE: 1999-11-16
PRIOR APPLICATION NUMBER: 60/198,568
PRIOR FILING DATE: 2000-04-20
CURRENT APPLICATION NUMBER: 60/166,071

PRIOR FILING DATE: 1999-11-17
PRIOR APPLICATION NUMBER: 60/166,678
PRIOR FILING DATE: 1999-11-19
PRIOR APPLICATION NUMBER: 60/173,396
PRIOR FILING DATE: 1999-12-28
PRIOR APPLICATION NUMBER: 60/184,129
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: 60/185,421
PRIOR FILING DATE: 2000-02-28
PRIOR APPLICATION NUMBER: 60/185,554
PRIOR FILING DATE: 2000-02-28
PRIOR APPLICATION NUMBER: 60/186,530
PRIOR FILING DATE: 2000-03-02
PRIOR APPLICATION NUMBER: 60/186,811
PRIOR FILING DATE: 2000-03-03
PRIOR APPLICATION NUMBER: 60/188,114
PRIOR FILING DATE: 2000-03-09
PRIOR APPLICATION NUMBER: 60/190,310
PRIOR FILING DATE: 2000-03-17
PRIOR APPLICATION NUMBER: 60/190,800
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/201,190
PRIOR FILING DATE: 2000-05-02
PRIOR APPLICATION NUMBER: 60/203,111
PRIOR FILING DATE: 2000-05-08
PRIOR APPLICATION NUMBER: 60/207,094
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 190
SOFTWARE: PatentIn version 3.1
SEQ ID NO 62
LENGTH: 143
TYPE: PRT
ORGANISM: Homo sapiens
US-10-130-469-62

Query Match 23.9%; Score 470; DB 6; Length 143;
Best Local Similarity 58.5%; Pred. No. 9, 2e-35;
Matches 83; Conservative 29; Mismatches 28; Indels 2; Gaps 1;

QY 1 MANTSHADNIIQNTSP--LTAFKLTSLGFIIGSVGNLISILVCKDTHRAPYF 58
DB 1 MANTGEPEEVSGALSPSASATYKLVLTGLIMCVSLAGNALISLVKRALHRAKYF 60
QY 59 LLDCCSDILRSALICFPFVNSVKNSTWTYGLTCKVIAFLGVLSCEFTAFMLFCISVT 118
DB 61 LLDCLADGIRSAVCFPPVYASVRHGSSWTFSAISCKIVAFMAVLCFHFAPMLFCISVT 120
QY 119 RYLAIAHHRFYTKRLTFWTCLAVT-----CM-VWTLVSMAFPP 140
DB 121 RYMAIAHHRFYAKRMTLMTWCXAASAMXGCLPMPFHLTLTWAP 142

RESULT 8
US-10-130-469-30
Sequence 30, Application US/10130469
GENERAL INFORMATION:
APPLICANT: Vogell, Gabriel
APPLICANT: Huff, Rita
APPLICANT: Sejlitz, Torsten
APPLICANT: Lind, Peter
APPLICANT: Slightom, Jerry
APPLICANT: Schellin, Kathleen
APPLICANT: Bannigan, Chris
APPLICANT: Ruff, Valerie
APPLICANT: Kayles, Paul
APPLICANT: Wood, Linda
APPLICANT: Parodi, Luis
APPLICANT: Hiesch, Ronald
TITLE OF INVENTION: Novel G Protein Coupled Receptors
FILE REFERENCE: 237.PIUS
CURRENT APPLICATION NUMBER: US/10/130,469
PRIOR FILING DATE: 2002-05-16

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PRIOR APPLICATION NUMBER: 60/165,838
PRIOR FILING DATE: 1999-11-16
PRIOR APPLICATION NUMBER: 60/198,568
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: 60/166,071
PRIOR FILING DATE: 1999-11-17
PRIOR APPLICATION NUMBER: 60/166,678
PRIOR FILING DATE: 1999-11-19
PRIOR APPLICATION NUMBER: 60/173,396
PRIOR FILING DATE: 1999-12-28
PRIOR APPLICATION NUMBER: 60/184,129
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: 60/185,421
PRIOR FILING DATE: 2000-02-28
PRIOR APPLICATION NUMBER: 60/185,554
PRIOR FILING DATE: 2000-02-28
PRIOR APPLICATION NUMBER: 60/186,530
PRIOR FILING DATE: 2000-03-02
PRIOR APPLICATION NUMBER: 60/186,811
PRIOR FILING DATE: 2000-03-03
PRIOR APPLICATION NUMBER: 60/188,114
PRIOR FILING DATE: 2000-03-09
PRIOR APPLICATION NUMBER: 60/190,310
PRIOR FILING DATE: 2000-03-17
PRIOR APPLICATION NUMBER: 60/190,800
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/201,190
PRIOR FILING DATE: 2000-05-02
PRIOR APPLICATION NUMBER: 60/203,111
PRIOR FILING DATE: 2000-05-08
PRIOR APPLICATION NUMBER: 60/207,094
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 190
SOFTWARE: PatentIn version 3.1
SEQ ID NO: 30
LENGTH: 106
TYPE: PRT
ORGANISM: Homo sapiens
US-10-130-469-30

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Query Match 17.2% Score 337.5; DB 6; Length 106;
Best Local Similarity 59.2%; Pred. No. 5.1e-23;
Matches 61; Conservative 13; Mismatches 28; Indels 1; Gaps 1;

QY 250 GTPPTLLGIRONANTTGRRLVLDEFKMEKRISRMFYIMTFLLTLMGPYLVACYWY 309
  |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 GMPPTLLGIRONGHAA-S-RLLGMDVEKGEKLGKRMFYITLLFLLMSPYLVACYWY 59
  |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 310 FARGPVPCGFELTAAYWMSFAQAGINPVCIFSNRELRCFST 352
  |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 60 FVKACAVPHRYLATAYWMSFAQAAVNYCFLNKLKLCIRT 102
  |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 9
US-10-176-255-31
Sequence 31, Application US/10176255
GENERAL INFORMATION:
APPLICANT: Behan, Dominic P.
APPLICANT: Chalmers, Derek T.
APPLICANT: Liaw, Chen W.
APPLICANT: Russo, Joseph F.
APPLICANT: Thomsen, William J.
TITLE OF INVENTION: Non-Endogenous, Constitutively Activated Human Serotonin Receptor
FILE REFERENCE: AREN-0328
CURRENT APPLICATION NUMBER: US/10/176,255
CURRENT FILING DATE: 2002-06-19
PRIOR APPLICATION NUMBER: 09/060,188
PRIOR FILING DATE: 1998-04-14
PRIOR APPLICATION NUMBER: 09/767,013
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 09/292,072

```

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PRIOR FILING DATE: 1999-04-14
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn version 3.1
SEQ ID NO 31
LENGTH: 478
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: synthetic construct
US-10-176-255-31

```

```

Query Match 13.5% Score 264.5; DB 6; Length 478;
Best Local Similarity 23.9%; Pred. No. 8.4e-16;
Matches 83; Conservative 61; Mismatches 153; Indels 51; Gaps 9;

QY 30 IIGVSVGNLLISILVVKDTHRAPYVFLDLCCSDILRSACPPFVNSKNGSTWY 89
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 84 VIILTIAGNLIIVMAVSEKTLQNTNTFLMSLAIDMLGELVMPVSMITLTYGYRPL 143
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 90 GTLCKVIAFLGVLSCFTAFMLFCISVTRYLAIA---HHRFYKRLFTWCLAVTCY 145
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 144 PSKLCAYIYLDVLFSTASIMHLCAISDRYVAIQNPITHSRFNSRTAFELKIA----V 199
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 146 WTLVNAAF-PYLDVGYSTIREDOCTPOHRSFRANDSLGFMILLALILATOLVYIK 204
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 200 WTISVGISMPILVFGLODSKVFKEGSCLDADNDNVLIGSEFSPFIPILTIMYTYELTIK 259
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 205 L-----IFEVHRRRMRKMP---VOFVAASQMTFPGASGOAANWLAGEFGRTPT 256
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 260 VLRRQALMLHGHTEEPGLSLDLCKCKRN-----TAEEENSAN----- 299
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 257 LGIRONANTTGRRL-----VLDEFKMEKRISRMFYIMTFLLTLMGPYLVACYWY 309
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 300 ---PNDONARRRRKKRBRGTMQAINNERKASKVGIYFELVVMCMCPFIINNAV 355
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 310 FAR---GPVVGGLTAAYWMSFAQAGINPVCIFSNRELRCFST 354
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 356 ICKSCNEDYIGALLNFWWIGYLSAVNPVYTLFNKRYRAFSNYL 403
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

```

```

RESULT 10
US-10-176-255-25
Sequence 25, Application US/10176255
GENERAL INFORMATION:
APPLICANT: Behan, Dominic P.
APPLICANT: Chalmers, Derek T.
APPLICANT: Liaw, Chen W.
APPLICANT: Russo, Joseph F.
APPLICANT: Thomsen, William J.
TITLE OF INVENTION: Non-Endogenous, Constitutively Activated Human Serotonin Receptor
FILE REFERENCE: AREN-0328
CURRENT APPLICATION NUMBER: US/10/176,255
CURRENT FILING DATE: 2002-06-19
PRIOR APPLICATION NUMBER: 09/060,188
PRIOR FILING DATE: 1998-04-14
PRIOR APPLICATION NUMBER: 09/767,013
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 09/292,072
PRIOR FILING DATE: 1999-04-14
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn version 3.1
SEQ ID NO 25
LENGTH: 470
TYPE: PRT
ORGANISM: Homo sapiens
US-10-176-255-25

Query Match 13.1% Score 258; DB 6; Length 470;
Best Local Similarity 24.7%; Pred. No. 3.2e-15;
Matches 89; Conservative 63; Mismatches 155; Indels 54; Gaps 12;

```


OY 15 LSPALFALKLSLGF-----IIGVSVVGNLLISILVKKDKTLHRAPIYELLIDCCSDI 67
 DB 61 LSPSCSLHLQCKNMSALLTAVIILITIAIGNITLIVAVSLERKLOKNTNFTLMSLAIDM 120
 OY 68 LRSALCFPVFVSVANGSTWITGILCKYIAFLGVLSCHFTAMLCISTRTILATA--- 124
 DB 121 LIGFLVMPVSMULTILYGYWMPKSKCAWIKLDVLESTASIMHLCAISIDRYAVALONPL 180
 OY 125 -HHREYTKLFTWGLAVICWMTLSVAMAF-PVLDVGTSPIREDOCTFQHRSPRAN 182
 DB 181 HHSRNSRKALKIIA---WVTISVGISMPVPGLODDSKVFEKSGCL-----AD 230
 OY 183 DSLGEMLLALITLATQVLVYLKLFVHDKRKKPVQVAAVSONMTFHGASGQAAN 242
 DB 231 DN-EVLISFVSFPLITIVITVFL-----TIKSLQKATLC-----VSDIGTRA 275
 OY 243 WLAGRGCTPTPLIGI-----KQANNTGRRRLVLDLFEKMEKRISRYFTYITFL 293
 DB 276 KLASFSF--LPOSSLSSEKLFQRSIHREPGSYGR--TMOSSISNEOKACKVIGIVFL 330
 OY 294 FLITNGPYLVACYWRYEAR---GPVVPGEFLTAAMVMSFAQAGINPVCIFSRRLRCF 350
 DB 331 FVVMCPEFITIMAVICKESCNEVDYIGALINFTVWIGILSAVNPLVITLFEKTRSAF 390
 OY 351 S 351
 DB 391 S 391

RESULT 11
 US-10-127-940-7
 ; Sequence 7, Application US/10127940
 ; GENERAL INFORMATION:

APPLICANT: Kopin, Alan S.

TITLE OF INVENTION: ASSAY FOR NON-PEPTIDE AGONISTS TO
 PEPTIDE HORMONE RECEPTORS

NUMBER OF SEQUENCES: 23

CORRESPONDENCE ADDRESS:

ADDRESSEE: Clark & Elbing LLP

STREET: 176 Federal Street

CITY: Boston

STATE: MA

COUNTRY: USA

ZIP: 02110

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Fastseq version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/127,940

FILING DATE: 23-Apr-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/076,510

FILING DATE: 12 MAY 1998

APPLICATION NUMBER: 08/570,157

FILING DATE: 11-DEC-1995

ATTORNEY/AGENT INFORMATION:

NAME: Clark, Paul T.

REGISTRATION NUMBER: 30,162

REFERENCE/DOCKET NUMBER: 00398/109002

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617/428-0200

TELEFAX: 617/438-7045

TELEX: <Unknown>

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 453 amino acids

TYPE: amino acid

STRANDEDNESS: Not Relevant

TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 7:
 US-10-127-940-7

Query Match 13.18; Score 257.5; DB 6; Length 453;
 Best Local Similarity 24.18; Pred. No. 3.4e-15;
 Matches 91; Conservative 63; Mismatches 170; Indels 53; Gaps 9;

OY 16 SPLAFALKLSLGF-----IIGVSVVGNLLISILVKKDKTLHRAPIYELLIDCCSDI 75
 DB 64 SDLNLWRIWYVIFLISVFGNTLITLVNMRRLTNTNSFLSLASDLMAVAVLQMP 123
 OY 76 FVF--NSKNGSTWITGILCKYIAFLGVLSCHFTAMLCISTRTILATAHHHFFYTKRL 133
 DB 124 FTILPNLMEN---FIFBEVICRAAAYTMGLSVSTNLVAISIERYSALONPLXSRWQ 180
 OY 134 TFWTCLAVICWMTLSVAMAFPPVLDVGYTSFIEE---DOCTFQHRSPRANSLGFM 189
 DB 181 TRSHAYRVIAATWYLSIIMIPVLYNKTVPKMDRVRVGHQCLVWPSKOVQOA-WYVL 239
 OY 190 LIALILATQVLVYLKLFVHDKRKKPVQVAAVSONMTFHGASGQAANMLAGRCR 249
 DB 240 LTLTLEFPQVVMV-VAYGLISRELRYGIDPEMDLNEAKHNGVS----- 285
 OY 250 GPTPEPTL-----LGIKONANTTGRRLVLDLFEKME-----KRISR 285
 DB 286 --TPTTIPSGDEGDCGCIQYTKRNTNEMSTLTPSVCKMKORANINSEATLMKKRYIR 343
 OY 286 MEYIMTFLEFLMGPIYVACYWRYEAR---ARGPVVPGEFLTAAMVMSFAQAGINPVCIF 342
 DB 344 MLIVYAMFICWMPPIVAVMTWKADELAFNTLTGAPISFIHLSYSACVNPLIYCFM 403
 OY 343 NRELRCFSTLTYCR 359
 DB 404 NKRFKALGTFSCKR 420

RESULT 12
 US-10-176-255-33

; Sequence 33, Application US/10176255

; GENERAL INFORMATION:

APPLICANT: Behan, Dominic P.

APPLICANT: Chalmers, Derek T.

APPLICANT: Liaw, Chen W.

APPLICANT: Russo, Joseph F.

APPLICANT: Thomsen, William J.

TITLE OF INVENTION: Non-Endogenous, Constitutively Activated Human Serotonin Recept

FILE REFERENCE: AREN-0328

CURRENT APPLICATION NUMBER: US/10/176,255

CURRENT FILING DATE: 2002-06-19

PRIOR APPLICATION NUMBER: 09/060,188

PRIOR FILING DATE: 1998-04-14

PRIOR APPLICATION NUMBER: 09/767,013

PRIOR FILING DATE: 2000-12-22

PRIOR APPLICATION NUMBER: 09/292,072

PRIOR FILING DATE: 1999-04-14

NUMBER OF SEQ ID NOS: 33

SOFTWARE: PatentIn version 3.1

SEQ ID NO 33

LENGTH: 478

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: synthetic construct

US-10-176-255-33

Query Match 13.18; Score 256.5; DB 6; Length 478;
 Best Local Similarity 23.98; Pred. No. 4.4e-15;
 Matches 83; Conservative 64; Mismatches 150; Indels 51; Gaps 11;

QY 30 IIGVAVGNLLISILVKDKTLHRAPIYFLDLCCSDILRSALCEPFVNSVKNGSTWY 89
 Db 84 VIILTAGNLIIVMAVSELEKKNATNFILMSLADMLGLFVMPVSMILITLYGYWPL 143
 QY 90 GTLCKVIAFLGVLSCEFHAFMLFCISVTRYLAIA---HHRYTKRLTFWTCIAVICY 145
 Db 144 PSKLCAMVITLDVLFSTASIMHLCAISLDRYVAIQNP IHSRFSNRTKAFKLTIA---V 199
 QY 146 WTLVSAMAP-PYLDVGYTSFIREDOCTQHHSFRANDS-LGFMILLAILLATQUL-VY 202
 Db 200 WTLVSAMAP-PYLDVGYTSFIREDOCTQHHSFRANDS-LGFMILLAILLATQUL-VY 202
 QY 203 L--KLIFVHRRKMKP---VOFVAASONTWTFHFGASGQAAMNLAEGFGPPPTL 256
 Db 260 VLRQAMLLHGTETPEPGLSLDFLCKCKRN-----TAEENSAN----- 299
 QY 257 LGRONANTTGRRL-----VLDEFKMKRISRMFYIMTFLTLMPYVACWRY 309
 Db 300 ----PNOQONARRKKRERPRGTQAINNERAKKVLGIVFVFLIMCPEFTINIMAV 355
 QY 310 FAR---GPVPGGFLTAAMVMSFQAQINPFCISNRELRCFSTTL 354
 Db 356 ICKESCNEVIGALLNVFVWIGLSSAVNPLVYTLFNKIRAFSNYL 403

RESULT 13
 US-10-166-101-8
 Sequence 8, Application US/10166101

GENERAL INFORMATION:
 APPLICANT: Weinshank, Richard L.
 APPLICANT: Branchek, Theresa
 APPLICANT: Hartig, Paul
 TITLE OF INVENTION: DNA Encoding A 5-HT1F Receptor And Uses Thereof
 FILE REFERENCE: 39318-C
 CURRENT APPLICATION NUMBER: US/10/166,101
 PRIOR FILING DATE: 2002-06-10
 PRIOR APPLICATION NUMBER: 09/246,075
 PRIOR FILING DATE: 1999-02-05
 PRIOR APPLICATION NUMBER: 08/483,222
 PRIOR FILING DATE: 1995-06-07
 PRIOR APPLICATION NUMBER: 08/117,006
 PRIOR FILING DATE: 1994-08-22
 PRIOR APPLICATION NUMBER: PCT/US93/00149
 PRIOR FILING DATE: 1993-01-08
 PRIOR APPLICATION NUMBER: 07/817,920
 PRIOR FILING DATE: 1992-01-08
 NUMBER OF SEQ ID NOS: 13
 SOFTWARE: PatentIn Ver. 2.0 - beta
 SEQ ID NO 8
 LENGTH: 470
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-166-101-8

Query Match 12.9%; Score 253.5; DB 6; Length 470;
 Best Local Similarity 24.8%; Pred. No. 8e-15;
 Matches 84; Conservative 61; Mismatches 147; Indels 47; Gaps 11;

QY 30 IIGVAVGNLLISILVKDKTLHRAPIYFLDLCCSDILRSALCEPFVNSVKNGSTWY 89
 Db 84 VIILTAGNLIIVMAVSELEKKNATNFILMSLADMLGLFVMPVSMILITLYGYWPL 143
 QY 90 GTLCKVIAFLGVLSCEFHAFMLFCISVTRYLAIA---HHRYTKRLTFWTCIAVICY 145
 Db 144 PSKLCAMVITLDVLFSTASIMHLCAISLDRYVAIQNP IHSRFSNRTKAFKLTIA---V 199
 QY 146 WTLVSAMAP-PYLDVGYTSFIREDOCTQHHSFRANDS-LGFMILLAILLATQUL-VY 202
 Db 200 WTLVSAMAP-PYLDVGYTSFIREDOCTQHHSFRANDS-LGFMILLAILLATQUL-VY 202
 QY 203 L--KLIFVHRRKMKP---VOFVAASONTWTFHFGASGQAAMNLAEGFGPPPTL 256
 Db 260 VLRQAMLLHGTETPEPGLSLDFLCKCKRN-----TAEENSAN----- 299
 QY 257 LGRONANTTGRRL-----VLDEFKMKRISRMFYIMTFLTLMPYVACWRY 309
 Db 300 ----PNOQONARRKKRERPRGTQAINNERAKKVLGIVFVFLIMCPEFTINIMAV 355
 QY 310 FAR---GPVPGGFLTAAMVMSFQAQINPFCISNRELRCFSTTL 354
 Db 356 ICKESCNEVIGALLNVFVWIGLSSAVNPLVYTLFNKIRAFSNYL 403

Db 252 ITYVL---TIKSLQKNTLTC-----VSDGTRAKLASFSR--LPQSSLSSEKLFQ 296
 QY 260 ----RONANTTGRRLVLDEFKMKRISRMFYIMTFLTLMPYVACWRYFAR--- 312
 Db 297 RSHREGSYGR---TMOISNEQKACKVLGIVFVFLVMMCPFTINIMAVICKESC 353
 QY 313 GPVPGGFLTAAMVMSFQAQINPFCISNRELRCFS 351
 Db 354 NEVIGALLNVFVWIGLSSAVNPLVYTLFNKIRAFSNYL 403

RESULT 14
 US-10-127-940-3
 Sequence 3, Application US/10127940

GENERAL INFORMATION:
 APPLICANT: Kopin, Alan S.
 APPLICANT: Belborn, Martin
 TITLE OF INVENTION: ASSAY FOR NON-PEPTIDE AGONISTS TO
 PEPTIDE HORMONE RECEPTORS
 NUMBER OF SEQUENCES: 23
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Clark & Elbing LLP
 STREET: 176 Federal Street
 CITY: Boston
 STATE: MA
 COUNTRY: USA
 ZIP: 02110
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: FastSeq version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/127,940
 FILING DATE: 23-Apr-2002
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/09/076,510
 FILING DATE: 12 MAY 1998
 APPLICATION NUMBER: 08/570,157
 FILING DATE: 11-DEC-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Clark, Paul T.
 REGISTRATION NUMBER: 30,162
 REFERENCE/DOCKET NUMBER: 00398/109002
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617/428-0200
 TELEFAX: 617/438-7045
 TELEX: <Unknown>
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 448 amino acids
 TYPE: amino acid
 STRANDEDNESS: Not Relevant
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 3:
 US-10-127-940-3

Query Match 12.9%; Score 253; DB 6; Length 448;
 Best Local Similarity 24.9%; Pred. No. 8.5e-15;
 Matches 102; Conservative 47; Mismatches 146; Indels 114; Gaps 16;

QY 22 IKTSLGFIIGVAVGNLLISILVKDKTLHRAPIYFLDLCCSDILRSALCEPFVNSV 81
 Db 56 IRTTLAVVIFLMSVGNMILVYLGSRRLTYTNFLSLAVSDLLAVACHPFTLPN 115
 QY 82 KNGSTWYGTGLCKVIAFLGVLSCEFHAFMLFCISVTRYLAIAHHRYTKRLTFWT---- 137
 Db 116 LMG-TFIFGVICKAVSYLMGVSYSYTLSTLVAIALERSALCR---PLQARVWQTRSH 170

RESULT **3**

JC7287
G-protein coupled receptor, SREB1 - human
C.Species: Homo sapiens (man)
C.Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 02-Sep-2000
C.Accession: Jc7287
R.Matsuomo, M.; Salto, T.; Takasaki, J.; Kamohara, M.; Sugimoto, T.; Kobayashi, M.; Tachibana, Y.
Biochem. Biophys. Res. Commun. 272, 576-582, 2000
Affile: An evolutionarily conserved G-protein coupled receptor family, SREB, expressed

C:Superfamily vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane p
F:34-57/Domain: transmembrane #status predicted <TM1>
F:71-93/Domain: transmembrane #status predicted <TM2>
F:107-139/Domain: transmembrane #status predicted <TM3>
F:126-134/Region: G protein-binding #status predicted
F:148-112/Domain: transmembrane #status predicted <TM4>
F:199-222/Domain: transmembrane #status predicted <TM5>
F:377-398/Domain: transmembrane #status predicted <TM6>
F:407-430/Domain: transmembrane #status predicted <TM7>
F:13-17/Binding site: carbohydrate (asn) (covalent) #status predicted
F:230-240,250,260/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #sta
F:355/Binding site: phosphate (Ser) (covalent) (by cAMP-dependent kinase) #status pre

Query Match	13.1%;	Score 257.5;	DB 2;	Length 476;
Best Local Similarity	21.6%;	Pred. No. 2e-15;		
Matches` 101;	Conservative 60;	Mismatches 173;	Indels 133;	Gaps 15


```

Oy 146 WTLSVMAAPF-PYLVDCTYSPIREDOCTFOHRSFRANDSLSEFMILLALITATOLUYLK 204
Db 200 WTISGVSNMIPPEFGLODDSVFKOGSCLL-----ADDN--FVLGSEYAAFEIPLTIMV 251
Oy 205 LIEFVHDRRMKRPVQVAAVSAQNMWTFHGPASGQAAMNLAFGGRPTPTLLGI----- 259
Db 252 ITYFL-----TIKSLQKRALIC-----VSDLSLRAKLASFSF--LPOSSLSEKLFQ 296
Oy 260 ----RQNAITGRRRLVLVDEFKMEKRISRFEYIMTFLEFLTMGPVLVACYWYFAR--- 312
Db 297 RSIHREPGSYTGR---TMOSSISNEOKACKVGIYEFLEFVVMCPFEITINIMAVICKESC 353
Oy 313 GPVVPGGFLAAVWMSFAQAGINPVCIFSNBELRCRPFSTLLYC--RKSRLP 363
Db 354 NEHVITALLVFWVWIGIGYLLSAVNPLVTLFNKTYSAFS-RTIQOCYKENRKP 405

RESULT 7
S13323
alpha-1A adrenergic receptor - Japanese medaka
C:Species: Oryzias latipes (Japanese medaka)
C:Date: 23-Jul-1997 #sequence_revision 01-Aug-1997 #text_change 17-Mar-1999
C:Accession: S13323
R:Yasuoka, A.; Abe, K.; Arai, S.; Emori, Y.
Eur. J. Biochem. 235, 501-507, 1996
A:Title: Molecular cloning and functional expression of the alpha-1-A-adrenoceptor of Me
A:Reference number: S13323, MIMD:96184522
A:Accession: S13323
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-477 <YAS>
A:Cross-references: EMBL:D63859
A:Note: It is uncertain whether Met-1 or Met-8 is the initiator
C:Superfamily: vertebrate rhodopsin

Query Match 12.9%; Score 252.5; DB 2; Length 477;
Best Local Similarity 24.0%; Pred. No. 5,6e-15;
Matches 90; Conservative 64; Mismatches 160; Indels 61; Gaps 12;

Oy 2 ANYSHADNILONSLPLAEFLKLSLGIIGV----SVGNLLISLLYKDKTLHRAPIY 57
Db 18 SNCSHV-----LAPELNFEVKAVALGMVLGIFLFGVIGNILVILSVCHRHLDQVTVY 70
Oy 58 FLIDLCSDILRSACRPF--VENSVKNGSTWTYGTLPCKVIAFLGVLSCFHTAFMFLCI 115
Db 71 FYVNLVADLLESSTVLPFSALFEIL--DRWFGFGEVFNIMAAVDVLCCTASIMSCVI 127
Oy 116 SVTRYLAIAHREFTKRLTEWTCIAVICMWTLSVMAAPPVL-----DVGYSEFIRE 168
Db 128 SVDRYIGVSPRLRPAIMTKRRALLAVMLWLVSIIISIGPLGKWEPADEDTYCKITE 187
Oy 169 EDOCTFOHRSFRANDSLGFMLLALILIALIATOLVYLKLIFFVHDRRMKRPVQVAAVSAQNM 228
Db 188 EP-----GYALFSAVGS--FYPLAIILIMACYRYV-----VAOKESRG 224
Oy 229 TFGHSPGASGQAAMNLAFGGRPTPTLLGIHQNAITGRRRLVLDDEFMEKRISRMFY 288
Db 225 LKSGQKTEKSDSEQVILIRMHGNTTVS-----EDEALRSTHTFALRLKTSREKKAANTLG 280
Oy 289 IMTFLEFLTMGPVLVACYWYFARGPVVPG-----GLTAAVWMSFAQAGINPVCIFSN 343
Db 281 IYVGCFLVCLWLPFL-----VLPIGSIPPAKRPDPTVFKITFWMLGVENSCINILTIYCSN 335
Oy 344 RELRRCFSTTL-LYC 357
Db 336 QEEKKAFFQSLGLGVHC 350

RESULT 8
S02011
serotonin receptor 2 - rat

```

N:Alternate names: 5-hydroxytryptamine receptor 2 (5-HTR2)
C:Species: Rattus norvegicus (Norway rat)
C>Date: 01-Dec-1969 #sequence_revision 01-Dec-1989,#text_change 13-Aug-1999
C:Accession: S02011
R:Pritchett, D.B.; Bach, A.W.J.; Wozny, M.; Taleb, O.; Dal Toso, R.; Shih, J.C.; Seet
EMBO J. 7, 4135-4140, 1988
A>Title: Structure and functional expression of cloned rat serotonin 5HT-2 receptor.
A:Reference number: S02011; MUID:69210797
A:Accession: S02011
A:Molecule type: mRNA
A:Residues: 1-449 <PR>
A:Cross-references: EMBL:X13971; NID:g57855; PION:CAA32150.1; PID:g57856
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 12.7%; Score 250; DB 2; Length 449;
Best Local Similarity 24.1%; Pred. No. 8-8e-15;
Matches 85; Conservative 67; Mismatches 151; Indels 50; Gaps 13;

OY 30 IIGVAVGNLLSILLVKDKTLHRAVYFLDLCSSDLISAICPEPVNSVKNGSTWTY 89
 |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 62 VIILTIAGNIIIVAMVSLEKLIKQNTNFELMSLAIDLMLGLVLVPMSMTITLYGYRPL 121
 |||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
OY 90 GLTCTKVIAFAGVLSCFITAFMFCISTRTIATA----HHRFYIKLTFTCLAVICMY 145
 |||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 122 PSKDCAIATIIDVLFETSTASIMHLCAISLDRYVAIONPIHSHFNFSRTAPFLKIIA---V 177
 |||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
OY 146 WTLSVAAFP--PVLGVGTYSFIREDDOCTPOHRSPFRANDSGFMILLALLAQTVLYLK 204
 |||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 178 WTISGISMPIPVFELQDSKYFKGSCLL-----ADDN--FVLISGFVAFPIPTIMV 229
 |||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
OY 205 LIEFYHDRKKMKPVQFAVASQMTFHCGPGASGQAANMLAGFGCRPPPTLLGI----- 259
 |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 230 ITYFL----TKISLQKEATLC-----VSDISTRAKLASFSF--LPQSLSSEKLQ 274
 |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
OY 260 ----KQNANTGRRLVLVDEFKMEKRISRKFYITFFLILMGVYLACWRRPAR--- 312
 |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 275 RSIHREPESYAGR--TWQISINEQACKYLGIVTFLEFVVMGCFFTTINMAVICKEESC 331
 |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 332 NENVIGALLNVFWIGYISSAVNPVLTLENKTYSAFS-RITQCQYENRKP 383
 |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

RESULT 9
JC2459
gastrin/cholecystokinin B receptor - rabbit
C:Species: Orcyctolagus cuniculus (domestic rabbit)
C>Date: 21-Feb-1995 #sequence_revision 05-Apr-1995 #text_change 20-Apr-2000
C:Accession: JC2459
R:Blandlitzki, C.; Song, I.; Yamada, T.
Biochem. Biophys. Res. Commun. 202, 947-953, 1994
A>Title: Molecular cloning and structural analysis of the rabbit gastrin/CCKB receptc
A:Reference number: JC2459; MUID:94324990
A:Accession: JC2459
A:Molecule type: mRNA
A:Residues: 1-452 <BLA>
A:Cross-references: GB:L31548; NID:g495663; PION:AAA31194.1; PID:g495665
C:Genetics:
C:Introns: 49/1; 133/1; 216/2; 273/1
C:Superfamily: neurokinin 1 receptor
C:Keywords: receptor; transmembrane protein.
F:56-79/Domain: transmembrane #status predicted <TM1>
F:85-104/Domain: transmembrane #status predicted <TM2>
F:130-149/Domain: transmembrane #status predicted <TM3>
F:169-187/Domain: transmembrane #status predicted <TM4>
F:217-237/Domain: transmembrane #status predicted <TM5>
F:339-359/Domain: transmembrane #status predicted <TM6>
F:381-400/Domain: transmembrane #status predicted <TM7>

Query Match 12.7%; Score 249; DB 2; Length 452;

Query Match

12.78; Score 249; DB 2; Length 452;

Best Local Similarity 25.0%; Pred. No. 1.1e-14;
Matches 100; Conservative 52; Mismatches 158; Indels 90; Gaps 15;

QY 22 LKLSGFIIGSVGNLISILVKKDKTLHRAPIYLLDCCDILRSACFPFVNSV 81
Db 54 IRLTLAVIFLMSVGNLILVIGLSRRRLRTVNAFLLSAVSDLLAVACMEFTLLPN 113
QY 82 KNGSTWTCGLTCKVIAFLGSCFHTAFMLFCISVTRYALAHNRRTLRFTWT---- 137
Db 114 LMG-FFIFETVICKAVSYLMGVSVSSTLSVAIALERYSAICR----PLQARVWQRRSH 168
QY 138 CLAVICMWTLSSVMAAF-PVLDVGYTSFIREED---OCTFOHRSFRANDSLGFMELLA 192
Db 169 AARVILATFLLSGLLMVPV-----YTAQPVGPRLQCVHMRPSARVQWTSVLLLL 223
QY 193 LIL-----LATQLYVKLIF-----VHRRKMK 216
Db 224 LFFVPPVMAVAVAGLISRELTLGLRPSDSSESQSRVROGGLPGGAAPVHONQRCR 283
QY 217 PVQFVAASQNTF-----HGPGASGOAANMLAGFGKGPFTPLIGIRONANTTGRRL 271
Db 284 PEAAGLEDGDCGYOLPNSRPLELSALTAPISGPGGPRP-----AQAKL 330
QY 272 LVLDKEMKMRISRMFYIMTFLETLIMGPYLVACYMVFARGP---VDPGFLTAVM 327
Db 331 LA-----KKRYRMILVIVLEFMCMLPYVSANTPRAF-DGFGAHRALSGAPISFIHL 383
QY 328 SFAQAGINPFCIFSRLRR-CEFTLLYCRKSRLEPREP 366
Db 384 SYASACVNPVLYCCFMRFRROACLDICARCC-----PRPP 418

RESULT 10

S40689
5-hydroxytryptamine 2 receptor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 13-Aug-1999
C:Accession: S40689
R:Yang, W.; Chen, K.; Lan, N.C.; Gallaher, T.K.; Shih, J.C.
J. Neurosci. Res. 33, 196-204, 1992
A:Title: Gene structure and expression of the mouse 5-HT2 receptor.
A:Reference number: S40689; MUID:93085774
A:Accession: S40689
A:Status: Preliminary
A:Molecule type: mRNA
A:Residues: 1-471 <YAN>
A:Cross-references: EMBL:S49542; NID:g261074; PIDN:ABA24369.1; PID:g261075
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 12.7%; Score 249; DB 2; Length 471;
Best Local Similarity 23.1%; Pred. No. 1.1e-14;
Matches 83; Conservative 65; Mismatches 148; Indels 64; Gaps 12;

QY 30 IIGSVVGNLISILVKKDKTLHRAPIYLLDCCDILRSACFPFVNSVNGSTWTY 89
Db 84 VILLIAGNIIIVMAVSEKRLQONATNYFLMSLADMLGLFVMPVSMITIIYGYRPL 143
QY 90 GLTCKVIAFLGVLSCFHTAFMLFCISVTRYALA----HHREYTRKLTFTWCLAVICW 145
Db 144 PSKLCAMVITLDVLFSTASIMHLCALISDRYVAIQPHHSRNSKTKAFKITA----V 199
QY 146 WTLSSVMAAF-PVLDVGYTSFIREDOCTFOHRSFRANDSLGFMELLALILATOLVYLK 204
Db 200 WTISGISMPIPVFGLODSDSKVFKESCL-----ADON--FVLIGSFVAFIPIPLIWI 251
QY 205 LIF-----VDRKMKAVQVVAASQWMTTHGPGASGOAANMLAGFG 248
Db 252 ITYFLLTISLQKATLCVSDLSSTRAKLSFSFL-----POSSLSSEKTLFORSIH 300
QY 249 RGPFPPTLLGIRONANTTGRRLVLVDKEMKMRISRMFYIMTFLETLIMGPYLVACYMR 308

Db 301 REP-----GSYAGR---TMSISNQRKCKVIGVIFLFLVYWMKCFEITINMA 346
QY 309 VFAR---GPVPGFLTAAVMMSFAQAGINPFCISNRELRCFSTLLYC--RKSRLP 363
Db 347 VICRESNENIGALLNFVWIGYLSAVNPLVYTLFPKRTSARS-RYIOQYENRKP 405

RESULT 11

S28058
serotonin receptor 5 - mouse
N:Alternate names: 5-hydroxytryptamine 5 receptor (5HT-5)
C:Species: Mus musculus (house mouse)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Sep-1999
C:Accession: S28058
R:Plassat, J.; Boschert, U.; Amalaky, N.; Hen, R.
EMBO J. 11, 4779-4786, 1992
A:Title: The mouse 5HT5 receptor reveals a remarkable heterogeneity within the 5HT1D
A:Reference number: S28058; MUID:9309851.
A:Accession: S28058
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-357 <PLA>
A:Cross-references: EMBL:218278
C:Superfamily: octopamine receptor type I
C:Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; tra

Query Match 12.7%; Score 248.5; DB 2; Length 357;
Best Local Similarity 24.6%; Pred. No. 9.4e-15;
Matches 87; Conservative 56; Mismatches 151; Indels 59; Gaps 12;

QY 18 LTAFL-EKLSGFIIGSVGNLISILVKKDKTLHRAPIYLLDCCDILRSACFP 75
Db 36 LSAFRVLVTLGLFLAATFTMLLVLATILKVFHRVPHNLVASMASDVLVAVLVP 95
QY 76 FVFSVANGSMTWTGTLCKVIAFLGSCFHTAFMLFCISVTRYALAHNRFTKRLTF 135
Db 96 LSLVHELSGRRWQGRRLQOLIMADVLCCTASIMNVAIALDRWSTIRHLEYTLRTRK 155
QY 136 WTCIAVICMWTLSSVMAAFPVLDVG---TYSFIREDOCTFOHRSFRANDSLG-FMELL 191
Db 156 RVSNVMLLTMALSTVLSLAPL-FGMEYTSSESEQVS-REPSYVSTVGAFYPL 213
QY 192 ALILATQLYLKLIFVHDR--KMRPVQFVAASQWMTTHGPGASGOAANMLAGFGR 249
Db 214 CVVLFFVWKIYIRBAKFRGSKTNSVPEAVEY-KNATQH----- 254
QY 250 GPPFPPTLLGIR-----QONATTGRRLVLVDKEMKMRISRMFYIMTFLETLIMGPYLV 303
Db 255 ---PQWFTVRHATVTPQTEGDTRRE-----QKEORALAMVIGILGVLCMFPEFV 303
QY 304 A-----CYMRVFARGPVPGFLTAAVMMSFAQAGINPFCISNRELRCF 350
Db 304 TELISPLCSMD-----VPAIMKSIPLWIGYSFNPFLITYAFNRYSAP 349

RESULT 12

A47430
gastrin/cholecystokinin receptor B, short splice form - human
N:Alternate names: CCK-B/gastrin receptor; cholecystokinin-B/gastrin receptor
C:Species: Homo sapiens (man)
C:Date: 25-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 20-Jun-2000
C:Accession: A47430; J01352; A46645; A48262
R:Ito, M.; Matsui, T.; Taniguchi, T.; Tsukamoto, T.; Murayama, T.; Arima, N.; Nakata, J. Biol. Chem. 268, 18300-18305, 1993
A:Title: Functional characterization of a human brain cholecystokinin-B receptor. A
A:Reference number: A47430; MUID:93352657
A:Accession: A47430
A:Status: Preliminary
A:Molecule type: not compared with conceptual translation
A:Residues: 1-447 <TTO>
A:Cross-references: GB:D13305; NID:g436039; PIDN:BAA02564.1; PID:g436040
A:Experimental source: brain

A>Note: sequence extracted from NCBI backbone (NCBIF:136448)
R:Pisegna, J.R.; de Weerth, A.; Huppel, K.; Wank, S.A.
Biochem. Biophys. Res. Commun. 189, 296-303, 1992
A>Title: Molecular cloning of the human brain and gastric cholecystokinin receptor. Stru

A:Accession: JCI352
A:Molecule type: mRNA
A:Residues: 1-447 <PIS>
A:Cross-references: GB:L04473; NID:g179997; PIDN:AAA35660.1; PID:g179998
A:Experimental source: Brain, gastric
R:Lee, Y.M.; Beinborn, M.; McBrine, E.W.; Lu, M.; Kolakowski Jr., L.F.; Kopin, A.S.
J. Biol. Chem. 268, 8164-8169, 1993
A>Title: The human brain cholecystokinin-B/gastrin receptor. Cloning and characterization
A:Reference number: A46645; MUID:93216795
A:Accession: A46645
A>Status: nucleic acid sequence not shown; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-447 <LEE>
A:Cross-references: GB:L08112; NID:g306488; PIDN:AAA35657.1; PID:g306489
A:Experimental source: brain
A>Note: sequence extracted from NCBI backbone (NCBIP:129156)
R:Sony, I.; Brown, D.R.; Miltshire, R.N.; Gantz, I.; Trent, J.M.; Yamada, T.
Proc. Natl. Acad. Sci. U.S.A. 90, 9085-9089, 1993
A>Title: The human gastrin/cholecystokinin type B receptor gene: alternative splice dono
A:Reference number: A48262; MUID:94022320
A:Accession: A48262
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-447 <RES>
A:Cross-references: GB:L10822; NID:g406075; PIDN:AAC37528.1; PID:g406076
A:Gene: GDB:CCCKBR
A:Cross-references: GDB:136457; OMIM:118445
A:Map position: 11p15.5-11p15.4
A:introns: 51/1; 135/1; 218/2; 271/1
C:Superfamily: neurokinin 1 receptor
C:Keywords: alternative splicing; G protein-coupled receptor; glycoprotein; hormone rec
F:57-81/Domain: transmembrane #status predicted <TM2>
F:91-116/Domain: transmembrane #status predicted <TM2>
F:131-150/Domain: transmembrane #status predicted <TM3>
F:171-192/Domain: transmembrane #status predicted <TM4>
F:219-243/Domain: transmembrane #status predicted <TM5>
F:334-354/Domain: transmembrane #status predicted <TM6>
F:369-392/Domain: transmembrane #status predicted <TM7>
F:7.30.36/binding site: carbohydrate (Asn) (covalent) #status predicted
F:82.154,300,442/binding site: phosphate (Ser) (covalent) #status predicted
F:127-205/disulfide bonds: status predicted
F:321/binding site: phosphate (Thr) (covalent) #status predicted

Query Match 12.6%, Score 247.5; DB 2; Length 447;
Best Local Similarity 24.7%; Pred. No. 1.5e-14;
Matches 101; Conservative 48; Mismatches 145; Indels 115; Gaps 16;

OY 22 LKLTSLGFTIGVSVGNLILSLVKDKTLHRAPYFLDLLCCSDLSALCEPFVENSV 81
:::| | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 56 IRITLYAVIETMSVGNNLIIVGLSRRLRTVTNAFLISLAVSDDLAAVACMPETLPD 115
:::| | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 82 KNQSWTWTGTLCVKIARLAVLVSCPHTFMELFCISVTTRYIAAHRRFTKRLTFYT 137
:::| | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 116 LMG-FEFIGTVICAKVSATLMGVSSVSTLSIALALERSACR---PLGARVWQTSSH 170
:::| | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 138 CLAVICMWTLTSVAAPF-PVLADVGTYSFIRED--QCFOHRSFRANDSIGMLILA 192
| | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 171 AARVYAIAWLISGLIMVYP-----YTVQPVGGRVQLCVHRMSASARYQVWSVLLLL 225
| | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 193 LIL-----LATOLVIKILF-----FYHDRRKMKPVQVF 221
| | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 226 LEFIPGVMAVAYGLISRELVLGTRFDGDSDSQSRYRNQGLGAHVHONGRCPE--T 283
| | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 222 AAVSON-----WFTHGPCASQAANNLAGRGCRGPPTPLLGINON 262
| | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 284 GAVGSDSGCTVQLEPRSPALELTALTADPGES-----GSRTQAKLLA--- 327
| | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 263 ANTGRRLVLDEKMKRISRMFYMTFFLLTMCYVLACVRYVARGP---VVPG 318
 Db 328 -----KKRYVRLMVLTVLEFLLCMLPEVYSANTWRAT-DGGCAHALSLG 369
 QY 319 GFLTAAMVMSFAQAGINDFPCIFSNRELRL-CEFTLLLYCKRSRLPREP 366
 Db 370 APIPIHLILSYASACVNPDLVYCCFMHRRFRQALCFRCARC-----PRRP 413
 RESULT 13
 A34863
 A:serotonin receptor 2 - rat
 N:Alternate names: 5-hydroxytryptamine receptor 2 (5-HT2)
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 22-May-1998
 C:Accession: A34863; A40574
 R:Julius, D.; Huang, K.N.; Livelli, T.J.; Axel, R.; Jessell, T.M.
 A:Title: The 5HT2 receptor defines a family of structurally distinct but functionally
 A:Reference number: A34863; MUID:90138991
 A:Accession: A34863
 A:Molecule type: mRNA
 A:Residues: 1-471 <JUL>
 A:Cross-references: GB:M30705
 R:Li, J.; Chen, Y.; Kozak, C.A.; Yu, L.
 Genomics 11, 231-234, 1991
 A:Title: The 5-HT2 serotonin receptor gene Htr-2 is tightly linked to Es-10 on mouse
 A:Reference number: A40574; MUID:92112222
 A:Accession: A40574
 A:Molecule type: mRNA
 A:Residues: 1-309, 'R', '311-471 <LIU>
 A:Cross-references: GB:M64867
 C:Superfamily: vertebrate rhodopsin
 C:Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane F

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OM protein - protein search, using sw model

Run on: July 19, 2002, 14:39:39 ; Search time 13.42 seconds

(without alignments)
1067.529 Million cell updates/sec

Title: US-09-698-419-14

Sequence: 1 MANYSHADNIIQNLSPITR.....STLLCYCRSRRLREPCV1 370

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1963	100.0	370	1	GP85_HUMAN
2	1865.5	95.0	371	1	GP85_BRARE
3	1339.5	68.2	387	1	SRB3_BRARE
4	1283.5	65.4	373	1	SRB3_HUMAN
5	1276.5	65.0	373	1	SRB3_RAT
6	998.5	50.9	375	1	GP85_HUMAN
7	989	50.4	377	1	GP85_RAT
8	989	50.4	379	1	GP85_MOUSE
9	257.5	13.1	453	1	CCR_XENIA
10	257.5	13.1	476	1	GRE1_BALAM
11	253.5	12.9	471	1	SH2A_HUMAN
12	253.5	12.9	471	1	SH2A_MACMU
13	253	12.9	471	1	SH2A_CRIGR
14	252.5	12.9	400	1	OPN3_MOUSE
15	251.5	12.9	470	1	ALIA_ORVIA
16	251.5	12.8	388	1	SH4_CAVPO
17	251.5	12.8	470	1	SH4_MOUSE
18	251	12.8	470	1	SH2A_PIG
19	250	12.7	471	1	SH2A_RAT
20	249	12.7	452	1	SH2A_RAT
21	249	12.7	471	1	SH2A_RABIT
22	248.5	12.7	357	1	SH5A_MOUSE
23	247.5	12.6	447	1	GA8R_HUMAN
24	244.5	12.5	387	1	DADR_MOUSE
25	244	12.4	428	1	B4AR_MELGA
26	243.5	12.4	388	1	SH4_HUMAN
27	243	12.4	452	1	GA8R_RAT
28	243	12.4	564	1	SH11_DROME
29	242.5	12.4	357	1	SH5A_RAT
30	241.5	12.3	436	1	CCR_MOUSE
31	241.5	12.3	460	1	SH2C_RAT
32	241	12.3	458	1	SH2C_HUMAN
33	239.5	12.2	357	1	SH5A_HUMAN

34	238	12.1	539	1	DOP2_DROME	024563 drosophila
35	237.5	12.1	515	1	ALAB_MESAU	P18841 mesocricetu
36	237	12.1	467	1	BIAR_BOVIN	09t96 bos taurus
37	236	12.0	454	1	GA8R_BOVIN	P79286 bos taurus
38	236	12.0	459	1	SH2C_MOUSE	P34968 mus musculus
39	235.5	12.0	453	1	GA8R_CANFA	P30552 canis famill
40	235	12.0	446	1	SH7_CAVPO	P50407 cavia porce
41	235	12.0	466	1	BIAR_RAT	P18090 rattus norv
42	234.5	11.9	387	1	DADR_RAT	P30729 rattus norv
43	234.5	11.9	392	1	BR54_BOMOR	P47751 bombina ori
44	233.5	11.9	402	1	OPN3_HUMAN	09hly3 homo sapien
45	233.5	11.9	406	1	SH4_RAT	062758 rattus norv

ALIGNMENTS

RESULT	ID	GP85_HUMAN	STANDARD	PRT	370 AA.
AC	09NPD1	09NPD1			
DT	16-OCT-2001	(Rel. 40, Created)			
DT	16-OCT-2001	(Rel. 40, Last sequence update)			
DT	16-OCT-2001	(Rel. 40, Last annotation update)			
DE	Probable G-protein-coupled receptor GPR85 (Super conserved receptor expressed in brain 2) (P4RCX1).				
GN	GP85 OR SREB2.				
OS	Homo sapiens (Human),				
OS	Mus musculus (Mouse), and				
OS	Rattus norvegicus (Rat).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.				
OX	NCBI_TaxID=9606, 10090, 10116;				
RN	[1]				
RC	SEQUENCE FROM N.A.				
RC	SPECIES-Human, and Mouse; SPRAIN-CD-1; TISSUE-Fetal brain, and Brain;				
RX	MEDLINE-20435311, PubMed-10978537;				
RA	Helander S., Schaller H.C., Wittenberger T.;				
RT	"The brain-specific G-protein coupled receptor GPR85 with identical protein sequence in man and mouse maps to human chromosome 7q31."				
RL	Biochim. Biophys. Acta 1493:269-272(2000).				
RN	[2]				
RC	SEQUENCE FROM N.A.				
RC	SPECIES-Human, and Rat; TISSUE-Brain;				
RX	MEDLINE-20294882; PubMed-10833454;				
RA	Matsumoto M., Saito T., Takasaki J., Kamohara M., Sugimoto T.;				
RT	"An evolutionarily conserved G-protein coupled receptor family, SREB, expressed in the central nervous system."				
RL	Biochem. Biophys. Res. Commun. 272:576-582(2000).				
RN	[3]				
RC	SEQUENCE FROM N.A.				
RC	SPECIES-Human; TISSUE-Amygdala;				
RA	Pousterka A., Wellenreuther R., Mewes H.-W., Well B., Wiemann S.;				
RT	Submitted (Mar-2000) to the EMBL/GenBank/DBJ databases.				
RN	[4]				
RC	SEQUENCE FROM N.A.				
RC	SPECIES-Rat; STRAIN-Sprague-Dawley;				
RA	Kim H., Park S., Kang Y., Kim C., Jeon J.;				
RT	Submitted (Nov-1999) to the EMBL/GenBank/DBJ databases.				
RL	- FUNCTION: ORPHAN RECEPTOR.				
CC	- TISSUE SPECIFICITY: Integral membrane protein (By similarity).				
CC	- TISSUE SPECIFICITY: IN HUMAN HIGHLY EXPRESSED IN BRAIN AND TESTIS.				
CC	LOWER LEVELS IN SMALL INTESTINE, PLACENTA AND SPLEEN. IN BRAIN				
CC	REGIONS, DETECTED IN ALL REGIONS TESTED, BUT SOMEWHAT LOWER LEVELS				
CC	IN THE CORPUS CALLOSUM, MEDULLA AND SPINAL CORD. IN THE MOUSE				
CC	EXCLUSIVELY EXPRESSED IN BRAIN.				
CC	- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration				
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -				
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DR EMBL: AF250237; AAF79956.1; -
DR EMBL: AB040800; BAA96646.1; -
DR EMBL: AL61959; CAB82307.1; -
DR EMBL: AF254416; AAF79959.1; -
DR EMBL: AB040803; BAA96649.1; -
DR EMBL: AF203907; AAG42284.1; -
DR MIM: 605188; -
DR MGD: MGI:1937851; GPR85; -
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm_1; 2.
DR PRINTS: PR00237; GPCRHHODPSN.
DR PROSITE: PS00237; G-PROTEIN_RECIP_F1_1; FALSE_NEG.
DR PROSITE: PS50262; G-PROTEIN_RECIP_F1_2; 1.
KM G-protein coupled receptor; Transmembrane; Glycoprotein;
KM Multigene family.
FT DOMAIN 1 25
FT TRANSMEM 26 46
FT DOMAIN 47 57
FT TRANSMEM 58 78
FT DOMAIN 79 96
FT TRANSMEM 97 117
FT DOMAIN 118 137
FT TRANSMEM 138 158
FT DOMAIN 159 188
FT TRANSMEM 189 209
FT DOMAIN 210 286
FT TRANSMEM 287 307
FT DOMAIN 308 313
FT TRANSMEM 314 334
FT DOMAIN 335 370
FT DISULFID 94 172
FT CARBOHYD 83 83
FT CARBOHYD 182 182
SQ SEQUENCE 370 AA; 41994 MW; 7B67A39F6166AEB CRC64;

Query Match 100.0%; Score 1963; DB 1; Length 370;
Best Local Similarity 100.0%; Pred. No. 3e-126;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1. MANYSHADNITLONLSPLATLKLTSIGFTIGSVGNLISILVKKDKTHRAHYEFL 60
DB 1 MANYSHADNITLONLSPLATLKLTSIGFTIGSVGNLISILVKKDKTHRAHYEFL 60
QY 61 DLCCSDILRSALICPEFVNSVKNSTWYTGTLCKVIAFLGVLSCFHTAFMFCISVTRY 120
DB 61 DLCCSDILRSALICPEFVNSVKNSTWYTGTLCKVIAFLGVLSCFHTAFMFCISVTRY 120
QY 121 LATAHHEFYKRLTFEMTCIANVCMVMTLSVMAAPPVLDVGTYSIRREDOCTPHRSFR 180
DB 121 LATAHHEFYKRLTFEMTCIANVCMVMTLSVMAAPPVLDVGTYSIRREDOCTPHRSFR 180
QY 121 LATAHHEFYKRLTFEMTCIANVCMVMTLSVMAAPPVLDVGTYSIRREDOCTPHRSFR 180
DB 121 LATAHHEFYKRLTFEMTCIANVCMVMTLSVMAAPPVLDVGTYSIRREDOCTPHRSFR 180
QY 181 ANSLGEMLLALILALATQVLYKLIFVHDKRKKPKQVFAAASQNTTFFGPGASGOAA 240
DB 181 ANSLGEMLLALILALATQVLYKLIFVHDKRKKPKQVFAAASQNTTFFGPGASGOAA 240
QY 241 ANNLAGEGSGPTPTLLGIRONANTTGRRLVLDEFEMKRISIMFYIMTFLLTNGP 300
DB 241 ANNLAGEGSGPTPTLLGIRONANTTGRRLVLDEFEMKRISIMFYIMTFLLTNGP 300
QY 301 YIVACYRVARAGVVGGLTAAVMSFAQAGINPFCISNRLKRCSTLLCYCKRS 360
DB 301 YIVACYRVARAGVVGGLTAAVMSFAQAGINPFCISNRLKRCSTLLCYCKRS 360
QY 361 RLREPRYCVI 370
DB 361 RLREPRYCVI 370

RESULT 2
ID GP85_BRAE STANDARD; PRT; 371 AA.
AC 091919;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Super conserved receptor expressed in brain 2.
GN SREB2.
OS Brachydanio rerio (zebrafish) (zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Cypriniformes; Cyprinidae; Danio.
OX NCBI_Taxid=7955;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-20294882; PubMed-10833454;
RA Matsumoto M., Saito T., Takasaki J., Kamohara M., Sugimoto T.,
RA Kobayashi M., Tadokoro M., Matsumoto S., Ohishi T., Furuchi K.;
RT "An evolutionarily conserved G-protein coupled receptor family, SREB,
RT expressed in the central nervous system."
RL Biochem. Biophys. Res. Commun. 272:576-582(2000).
CC -1- FUNCTION: ORPHAN RECEPTOR.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (by similarity).
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS..
CC -----
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CC or send an email to license@isb-sib.ch).

DR EMBL: AB040805; BAA96651.1; -
DR ZFIN: ZDB-GENE-000710-2; sreb2.
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm_1; 2.
DR PRINTS: PR00237; GPCRHHODPSN.
DR PROSITE: PS00237; G-PROTEIN_RECIP_F1_1; FALSE_NEG.
DR PROSITE: PS50262; G-PROTEIN_RECIP_F1_2; 1.
KM G-protein coupled receptor; Transmembrane; Glycoprotein;
KM Multigene family.
FT DOMAIN 1 26
FT TRANSMEM 27 47
FT DOMAIN 48 58
FT TRANSMEM 59 79
FT DOMAIN 80 96
FT TRANSMEM 97 117
FT DOMAIN 118 138
FT TRANSMEM 139 159
FT DOMAIN 160 189
FT TRANSMEM 190 210
FT DOMAIN 211 287
FT TRANSMEM 288 308
FT DOMAIN 309 321
FT TRANSMEM 322 342
FT DOMAIN 343 371
FT DISULFID 95 173
FT CARBOHYD 3 3
FT CARBOHYD 84 84
FT CARBOHYD 183 183
SQ SEQUENCE 371 AA; 41954 MW; F6B6175B3A348C2 CRC64;

Query Match 95.0%; Score 1865.5; DB 1; Length 371;
Best Local Similarity 93.8%; Pred. No. 1.2e-119;
Matches 348; Conservative 10; Mismatches 12; Indels 1; Gaps 1;

QY 1. MANYSHADNITLONLSPLATLKLTSIGFTIGSVGNLISILVKKDKTHRAHYEFL 59
DB 1 MANYSHADNITLONLSPLATLKLTSIGFTIGSVGNLISILVKKDKTHRAHYEFL 60

QY	60	LDLCCSDILRSALICPEPEVNSYKNSWTMYGLTTCVIAFLVLSCFHNFAFMFCISVTR	119
DB	61	LDLCCSDILRSALICPEPEVNSYKNSWTMYGLTTCVIAFLVLSCFHNFAFMFCISVTR	120
QY	120	YLAIHHRYETKRLTFWMLCLAVICMWMLTSLVMAAPFPVLDVGYSEFIREDDCTFOHRSE	179
DB	121	YLAIHHRYETKRLTFWMLCLAVICMWMLTSLVMAAPFPVLDVGYSEFIREDDCTFOHRSE	180
QY	180	RANSLGFMILLALILATQVLYLKLIFFVHDRKKRPVQVAAVSONTFHGPGASGA	239
DB	181	RANSLGFMILLALILATQVLYLKLIFFVHDRKKRPVQVAAVSONTFHGPGASGA	240
QY	240	AANWLAGSGRGCTPTLIGIRONANTGRRRLVLDDEFMEKRISMEYIMTFLPTLWG	299
DB	241	AANWLAGSGRGCTPTLIGIRONANTGRRRLVLDDEFMEKRISMEYIMTFLPTLWG	300
QY	300	PLVACVYMWVFARGVNVGEGFLTAAVWMSFAQAGINPEVCISNRLRRCFSTLLCYCKR	359
DB	301	PLVACVYMWVFARGVNVGEGFLTAAVWMSFAQAGINPEVCISNRLRRCFSTLLCYCKR	360
QY	360	SRLEPPICVI 370	
DB	361	SRLEPPICVI 371	
RESULT	3		
SRB3_BRARE		STANDARD: PRT: 387 AA.	
ID	SRB3_BRARE		
AC	Q91918;		
DT	16-OCT-2001 (Rel. 40, created)		
DT	16-OCT-2001 (Rel. 40, last sequence update)		
DT	16-OCT-2001 (Rel. 40, last annotation update)		
DE	Super conserved receptor expressed in brain 3.		
GN	SRB3.		
OS	Brachydanio rerio (zebrafish) (Zebra danio).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;		
OC	Cypriniformes; Cyprinidae; Danio.		
OX	NCBI_TaxID=7955;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=20294882; PubMed=10833454;		
RA	Matsumoto M., Saito T., Takasaki J., Kamohara M., Sugimoto T.,		
RA	Kobayashi M., Tadokoro M., Matsumoto S., Ohishi T., Furuchi K.;		
RT	"An evolutionarily conserved G-protein coupled receptor family, SRB3,		
RL	Biochem. Biophys. Res. Commun. 272:576-582(2000).		
CC	-1- FUNCTION: ORPHAN RECEPTOR.		
CC	-1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).		
CC	-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.		
CC	-----		
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CC	or send an email to license@sdb-stb.ch).		
CC	-----		
DR	EMBL; AB040806; BAA96652.1; -		
DR	ZFIN; ZDB-GENE-000710-1; srebb.		
DR	InterPro: IPR000276; GPCR_Rhodopsn.		
DR	Pfam: PF00001; 7tm.1.1;		
DR	PRINTS; PRO0237; GPCRHHODOPS.		
DR	PROSITE; PS00237; G-PROTEIN_RECEP_FL_1; FALSE_NEG.		
DR	G-PROSITE; PS0262; G-PROTEIN_RECEP_FL_2; 1.		
KW	G-protein coupled receptor; Transmembrane; Glycoprotein;		
KW	Multigene family.		
FT	DOMAIN 1	40	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM 41	61	1 (POTENTIAL).
FT	DOMAIN 62	87	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM 88	108	2 (POTENTIAL).

Query Match	Best Local Similarity	Score	DB 1;	Length	387;
Matches 233; Conservative	65.38;	Fred. No. 4.6e-84;	Mismatches 59;	Indels 3;	Gaps 2
DOMAIN 109	111	EXTRACELLULAR (POTENTIAL).			
FT TRANSMEM 112	132	3 (POTENTIAL).			
FT DOMAIN 133	153	CYTOPLASMIC (POTENTIAL).			
FT TRANSMEM 154	174	4 (POTENTIAL).			
FT DOMAIN 175	202	EXTRACELLULAR (POTENTIAL).			
FT TRANSMEM 203	223	5 (POTENTIAL).			
FT DOMAIN 224	301	CYTOPLASMIC (POTENTIAL).			
FT TRANSMEM 302	322	6 (POTENTIAL).			
FT DOMAIN 323	335	EXTRACELLULAR (POTENTIAL).			
FT TRANSMEM 357	387	7 (POTENTIAL).			
FT DOMAIN 357	387	CYTOPLASMIC (POTENTIAL).			
FT DISULFID 110	188	BY SIMILARITY			
FT CARBOHYD 5	5	N-LINKED (GLCNAC. . .) (POTENTIAL).			
FT CARBOHYD 198	198	N-LINKED (GLCNAC. . .) (POTENTIAL).			
FT CARBOHYD 387 AA;	43409 MM;	5B094EFD4120871 CRC64;.			
SEQUENCE					
Query Match	68.2%;	Score 1339.5;	DB 1;	Length 387;	
Best Local Similarity	65.38;	Fred. No. 4.6e-84;	Mismatches 59;	Indels 3;	Gaps 2
Matches 233; Conservative	62;	Mismatches 59;	Indels 3;	Gaps 2	
16 SPLTFEKLKTSGLFIFGVNGLISILVYDKTLHRAVYFLDLCSDILRSACIP 75					
1 SAVSYKVLVLGLLITSLVGNLVSLVLRDLRHLKRPYFLDLCLADIIRSAVCP 91					
32					
76 EVNSVKNKSTWYGYTLCKVIAFLGLVLSCEPTAFMLFCISVTRYAIATAHRRPYTKRLTF 135					
32 FYLVSKNSAMTYSVLSCKVAFMAVLECFPAAMLFICISTRYMALAHHRFYSKRMTF 151					
136 WTGLAVICWMTLSAAMAPRYLDVGYTSFIEEDOCYFOHRSFRANDSLGFMILLALTL 195					
152 WTCVAVVCCWMTLSVAAAFPPVDFDGTAKFIEEDOCIFEHRYFRFANOTLIGFMLMLAVLI 211					
196 LATOLVYLKLFYVDHRRKMKPVGVAAVSONWTFHGPASOAAANMAGRGGRPTPT 255					
212 LATHVVMKLLFEKHKRMKPVQWPAISQWTFHGPATSOAAANMAGRGGRPTPT 271					
256 ILGIRONANTTGRRLRLVLEEFKMKKRISRMVYIMTFELITMAGVILVACYRVRFARGPV 315					
272 ILGIRONLHNG-NRRLILGEEFKAKOLGRMYITLTFVLVMSYIAYACRYRVVAKCT 330					
316 VEGFLVAAVWMSFPAQAGINPFVCFISNRELRCFSTLLYCRKS-RLPREPCVI 370					
331 IPHRYLSTVWMSFPAQAGINPFICFLNLDKKGLLHLPPCCRRPPOLPREPCVM 387					
RESULT 4					
SRB3_HUMAN	STANDARD;	PRT;	373 AA.		
AC	Q9NS66;				
DT	16-OCT-2001 (Rel. 40, Created)				
DT	16-OCT-2001 (Rel. 40, Last sequence update)				
DT	16-OCT-2001 (Rel. 40, Last annotation update)				
DE	Super conserved receptor expressed in brain 3.				
GN	SRB3.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Brain;				
RX	MEDLINE=20294882; PubMed=10833454;				
RA	Matsunoto M., Saito T., Takasaki J., Kanohara M., Sugimoto T.,				
RA	Kobayashi M., Tadokoro M., Matsunoto S., Onishi T., Furutachi K.,				
RT	"An evolutionary conserved G-protein coupled receptor family, SRB3,				
RT	expressed in the central nervous system."				
RL	Biochem. Biophys. Res. Commun. 272:576-582(2000).				
CC	-1- FUNCTION: ORPHAN RECEPTOR.				
CC	-1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).				
CC	-1- TISSUE SPECIFICITY: EXPRESSED AT HIGH LEVELS IN BRAIN AND OVARY.				
CC	LOWER LEVELS IN SMALL INTESTINE. IN BRAIN REGIONS, DETECTED IN ALL				
CC	REGIONS TESTED. HIGHEST LEVELS IN THE CEREBELLUM AND CEREBRAL				

CORTEX.

-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

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CC EMBL: AB040801; BAA96647.1; -
 DR MIM: 300253; -
 DR InterPro: IPR000276; GPCR_Rhodopsn.
 DR Pfam: PF00001; 7tm_1; 1.
 DR PRINTS: PR00237; GPCR_RHODOPSIN.
 DR PROSITE: PS00237; G-PROTEIN_RECEP_FL_1; FALSE_NEG.
 DR PROSITE: PS50262; G-PROTEIN_RECEP_FL_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;
 KW Multigene family.

FT DOMAIN 1 26
 FT TRANSMEM 27 47
 FT TRANSMEM 48 59
 FT TRANSMEM 60 80
 FT TRANSMEM 81 97
 FT TRANSMEM 98 118
 FT TRANSMEM 119 139
 FT TRANSMEM 140 160
 FT TRANSMEM 161 188
 FT TRANSMEM 189 209
 FT TRANSMEM 210 287
 FT TRANSMEM 288 308
 FT TRANSMEM 309 322
 FT TRANSMEM 323 343
 FT TRANSMEM 344 373
 FT DISULFID 96 174
 FT CARBOHYD 184 184
 FT CARBOHYD 184 184
 SQ SEQUENCE 373 AA: 41481 MW: 8A227F914C9D8358 CRC64;

Query Match 65.4%; Score 1283.5; DB 1; Length 373;
 Best Local Similarity 62.3%; Pred. No. 2.7e-80;
 Matches 233; Conservative 56; Mismatches 80; Indels 5; Gaps 3;

QY 1 MANYSHADNIIQNLSP--LTAFLKLTSLGFIIGSVGNLISILVKKDTHRAPYF 58
 DB 1 MANTTGEPEVSGALSPSPASAYVKLVLLGLIMCVSLAGNAIISLVYKRALHAKAPYF 60
 QY 59 LLDLCCSDILRSALCEPFVNSVKNSTWYGTLTCKVIAFLGVLSCEHTAFMLFCISVT 118
 DB 61 LLDLCLADIRSAVCEPFVLASVRHSSWTFMSLCKIYAFMAVLCEFHAFMLFCISVT 120
 QY 119 RLTAIAHNFYKRLFTWCLAVICWVTLVSAMAPPLVDVSTYFIREDOCTQHR 178
 DB 121 RYMAIAHNFYKRLFTWCLAVICWVTLVSAMAPPLVDVSTYFIREDOCTQHR 180
 QY 179 FRANDSLGFMILLALITLITOLVYLKLFVHDKRKKPPOFAAASOMTFHGPASGQ 238
 DB 181 FRANDTLGFMILLALITLITOLVYLKLFVHDKRKKPPOFAAASOMTFHGPATGQ 240
 QY 239 AAANMLAGRGPTPEPTLLGIRONANTTGRRLVLDEFEKMERISRMFYIMTFLETL 298
 DB 241 AAANMLAGRGPTPEPTLLGIRONANTTGRRLVLDEFEKMERISRMFYIMTFLETL 299
 QY 299 GYLYACVYKRVARAGVYVGGELTAAVMSFQAGINPFYCISNDELRCFST--TL 356
 DB 300 SYIYACVYKRVARAGVYVGGELTAAVMSFQAGINPFYCISNDELRCFST--TL 359
 QY 357 CRKSLRPREPYCVI 370
 DB 360 TGGAPAPRPREPYCVI 373

RESULT 5

SRB3_RAT ID STANDARD: PRT; 373 AA.

AC 09JH2;
 DT 16-OCT-2001 (Rel. 40; Created)
 DT 16-OCT-2001 (Rel. 40; Last sequence update)
 DT 16-OCT-2001 (Rel. 40; Last annotation update)
 DT Super conserved receptor expressed in brain 3.
 DE SREB3.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_Taxid=10116;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=20294882; PubMed=10833454;
 RA Matsumoto M., Saito T., Takasaki J., Kamohara M., Sugimoto T.,
 RA Kobayashi M., Tadokoro M., Matsumoto S., Ohishi T., Furuchi K.,
 RT "An evolutionarily conserved G-protein coupled receptor family, SREB,
 RT expressed in the central nervous system."
 CC Blochem. Biophys. Res. Commun. 272:576-582(2000).
 CC -1- FUNCTION: ORPHAN RECEPTOR.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

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 CC or send an email to license@sib-sib.ch).

CC EMBL: AB040804; BAA96650.1; -
 DR InterPro: IPR000276; GPCR_Rhodopsn.
 DR Pfam: PF00001; 7tm_1; 1.
 DR PRINTS: PR00237; GPCR_RHODOPSIN.
 DR PROSITE: PS00237; G-PROTEIN_RECEP_FL_1; FALSE_NEG.
 DR PROSITE: PS50262; G-PROTEIN_RECEP_FL_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;
 KW Multigene family.

FT DOMAIN 1 26
 FT TRANSMEM 27 47
 FT TRANSMEM 48 59
 FT TRANSMEM 60 80
 FT TRANSMEM 81 97
 FT TRANSMEM 98 118
 FT TRANSMEM 119 139
 FT TRANSMEM 140 160
 FT TRANSMEM 161 188
 FT TRANSMEM 189 209
 FT TRANSMEM 210 287
 FT TRANSMEM 288 308
 FT TRANSMEM 309 322
 FT TRANSMEM 323 343
 FT TRANSMEM 344 373
 FT DISULFID 96 174
 FT CARBOHYD 184 184
 FT CARBOHYD 184 184
 SQ SEQUENCE 373 AA: 41511 MW: C06DEA2F0E88CAFS CRC64;

Query Match 65.0%; Score 1276.5; DB 1; Length 373;
 Best Local Similarity 62.3%; Pred. No. 8.1e-80;
 Matches 233; Conservative 55; Mismatches 81; Indels 5; Gaps 3;

QY 1 MANYSHADNIIQNLSP--LTAFLKLTSLGFIIGSVGNLISILVKKDTHRAPYF 58
 DB 1 MANTTGEPEVSGALSPSPASAYVKLVLLGLIMCVSLAGNAIISLVYKRALHAKAPYF 60
 QY 59 LLDLCCSDILRSALCEPFVNSVKNSTWYGTLTCKVIAFLGVLSCEHTAFMLFCISVT 118


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DB 61 LLDLCLADGIRSAICPPFVLASVHRSSWTFSLSCSIVAFMAVLFCEFHAAFMFCISVT 120
OY 119 RLTAIAHHRFYKRLTFWTCFLAVICWMTLSVMAPEPVLIDVGYTSIFREDOCTEQHRS 178
DB 121 RYMAIAHHRFYKRLMTLCAVICAAMTSLVMAPEPVDVGYTKFIREDOCTEQHRS 180
OY 179 FRANDSLGEMLLALLLTLTOLVYLLKLFVHRRKMKRPQFAVAASQNTFPGASGQ 238
DB 181 FRANDSLGEMLLAVMAATHAAYGRLLFEYHRRKMKRPQMPALISQNTFPGASGQ 240
OY 239 AAANMLAGCGRPTPTLLGIRONANTTGRRLVLDDEFKMERKISMFTYIMTEFLTM 298
DB 241 AAANMLAGCGRPTPTLLGIRONGHAAS-RLLGDEYKGEKOLGSMFTYIMTEFLTM 299
OY 299 GYLVAACYWRFVARGPVDFGLTAAVWMSFAQAGINPVCIFSNRELRCFST--TLLY 356
DB 300 SPYIVACYWRFVARGPVDFGLTAAVWMSFAQAGINPVCIFSNRELRCFST--TLLY 359
OY 357 CRKSLRPREPCVI 370
DB 360 TGGAPAPREPCVM 373

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RESULT 6
GPRS_HUMAN STANDARD; PRT; 375 AA.
ID GPRS_HUMAN
AC Q9NS67;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Probable G-protein-coupled receptor GPR27 (Super conserved receptor
  expressed in brain 1).
GN GPR27 OR SREB1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxId:9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE-20294882; PubMed-10833454;
RA Matsumoto M., Saito T., Takasaki J., Kamohara M., Sugimoto T.,
  Kobayashi M., Tadokoro M., Matsumoto S., Ohishi T., Furuichi K.;
  "An evolutionarily conserved G-protein coupled receptor family, SREB,
  expressed in the central nervous system.";
  Biochem. Biophys. Res. Commun. 272:576-582(2000).
RL 1. FUNCTION: ORPHAN RECEPTOR. POSSIBLE CANDIDATE FOR AMINE-LIKE G-
  PROTEIN COUPLED RECEPTOR.
CC 1. SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC 1. TISSUE SPECIFICITY: HIGHLY EXPRESSED AS A 3.0 KB TRANSCRIPT IN
  BRAIN, OVARY, TESTIS, HEART, PROSTATE AND PERIPHERAL LEUCOCYTES.
CC LOWER LEVELS IN PANCREAS AND SMALL INTESTINE. A 2.3 KB TRANSCRIPT
  WAS ALSO FOUND IN PERIPHERAL LEUCOCYTES. IN BRAIN REGIONS,
  DETECTED AS A 3.0 KB TRANSCRIPT IN ALL REGIONS TESTED. HIGHEST
  LEVELS IN THE CADATE NUCLEUS, PUTAMEN, HIPPOCAMPUS AND
  SUBTHALAMIC NUCLEUS. LOWEST LEVEL IN THE CEREBELLUM.
CC 1. SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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  CC or send an email to license@sib-sib.ch).
CC
DR EMBL, AB040799; BAA96645.1;
DR MM, 605187;
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR Pfam: PF00001; 7tm.1.1.
DR PRINTS: PR00237; GPCR_Rhodopsin.
DR PROSITE, PS00237; G-PROTEIN_RECPT_FL_1; FALSE_NEG.

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DR PROSITE: PS00262; G-PROTEIN_RECPT_FL_2; 1.
KM G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Multigene family.
FT DOMAIN 1 23 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 24 44 1 (POTENTIAL).
FT DOMAIN 45 55 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 56 76 2 (POTENTIAL).
FT DOMAIN 77 97 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 98 118 3 (POTENTIAL).
FT DOMAIN 119 139 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 140 160 4 (POTENTIAL).
FT DOMAIN 161 181 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 182 202 5 (POTENTIAL).
FT DOMAIN 203 285 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 286 306 6 (POTENTIAL).
FT DOMAIN 307 320 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 321 341 7 (POTENTIAL).
FT DOMAIN 342 375 CYTOPLASMIC (POTENTIAL).
FT DISULFID 95 171 BY SIMILARITY.
FT CARBOHYD 3 3 N-LINKED (GLCNAC... ) (POTENTIAL).
SQ SEQUENCE 375 AA; 39818 MW; E17AF3D86FD47204 CRC64;

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Query Match 50.94; Score 998.5; DB 1; Length 375;
 Best Local Similarity 55.28; Pred. No. 5.2e-61;
 Matches 190; Conservative 51; Mismatches 96; Indels 7; Gaps 3;

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OY 22 LKLTSLGFIIGSVVGNLISILVKKDKTLRAAYFLLDCCSDILSAICPPFVNSV 81
DB 20 LKLTSLGFIIGSVVGNLISILVKKDKTLRAAYFLLDCCSDILSAICPPFVNSV 79
OY 82 KNGSTWT--YGLTCKVIAFLVGLSCFHTAFMLFCISVTRYLAIAHHRFYKRLTWTG 138
DB 80 RRAAAGAPPAAGLCKLAFALFCFHAFLVGVTRYLAIAHHRFYKRLTWTG 139
OY 139 LA-VICWMTLSVMAPEPVLIDVGYTSIFIREDOCTQHRSFRANDSLGEMLLALLILA 197
DB 140 AAALVCAAMALALAAAPPPVLDGGDD--EDACALAEORDGAPGALGFLILLAVVGA 196
OY 198 TOLVYLKLFVHRRKMKRPQFAVAASQNTFPGASGQAAANMLAGCGRPTPTLL 257
DB 197 TOLVYLKLFVHRRKMKRPQFAVAASQNTFPGASGQAAANMLAGCGRPTPTLL 256
OY 258 GIRONANTTGRRLVLDDEFKMERKISMFTYIMTEFLTMGPYLVACYWRFVARGPV 317
DB 257 GIRAPGGRGARRLVLEERTKRLCKMFAVYLLFLMLGPYLVACYWRFVARGPV 316
OY 318 GGFLLTAVWMSFAQAGINPVCIFSNRELRCFSTTLLYCRKSR 361
DB 317 QAVLTASVWLTFAQAGINPVCIFSNRELRCFSTTLLYCRKSR 360
RESULT 7
GPRS_RAT STANDARD; PRT; 377 AA.
ID GPRS_RAT
AC Q9JUH3;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Probable G-protein-coupled receptor GPR27 (Super conserved receptor
  expressed in brain 1).
GN GPR27 OR SREB1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxId:10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE-20294882; PubMed-10833454;
RA Matsumoto M., Saito T., Takasaki J., Kamohara M., Sugimoto T.,
  Kobayashi M., Tadokoro M., Matsumoto S., Ohishi T., Furuichi K.;
  "An evolutionarily conserved G-protein coupled receptor family, SREB,

```

RT expressed in the central nervous system.";
 RL Blochem. Biophys. Res. Commun. 272:576-582(2000).
 RN [2]
 RP TISSUE SPECIFICITY.
 RX MEDLINE=98140132; PubMed=9479505;
 RA O'Dowd B.F., Nguyen T., Marchese A., Cheng R., Lynch K.R.,
 RA Heng H.H.O., Kolakowski L.F. Jr., George S.R.;
 RT "Discovery of three novel G-protein-coupled receptor genes".
 RL Genomics 47:310-313(1998).
 CC -1- FUNCTION: ORPHAN RECEPTOR. POSSIBLE CANDIDATE FOR AMINE-LIKE G-
 CC PROTEIN COUPLED RECEPTOR (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (by similarity).
 CC -1- TISSUE SPECIFICITY: EXPRESSED AS A 3.0 KB TRANSCRIPT, IN WHOLE
 CC BRAIN, HIPPOCAMPUS, STRIATUM, FRONTAL CORTEX, THALAMUS, PONS AND
 CC HYPOTHALAMUS. A LOWER MOLECULAR WEIGHT TRANSCRIPT WAS DETECTED IN
 CC ALL REGIONS EXAMINED, EXCEPT THE HYPOTHALAMUS.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC -----
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 CC -----
 CC EMBL; AB040802; BAA96648.1;
 CC InterPro: IPR000276; GPCR_Rhodpsn.
 DR Pfam: PF00001; 7tm.1; 1.
 DR PRINTS: PR00237; GPCRHOPOPSN.
 DR PROSITE: PS00237; G_PROTEIN_RECPT_FL_1; FALSE_NEG.
 DR PROSITE: PS50262; G_PROTEIN_RECPT_FL_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;
 KW Multigene family.
 FT DOMAIN 1 24
 FT TRANSMEM 25 45
 FT DOMAIN 46 56
 FT TRANSMEM 57 77
 FT DOMAIN 78 98
 FT TRANSMEM 99 119
 FT DOMAIN 120 140
 FT TRANSMEM 141 161
 FT DOMAIN 162 183
 FT TRANSMEM 184 204
 FT DOMAIN 205 287
 FT TRANSMEM 288 308
 FT DOMAIN 309 322
 FT TRANSMEM 323 343
 FT DOMAIN 344 377
 FT DISULFID 96 173
 FT CARBOHYD 3 3
 SQ SEQUENCE 377 AA; 39892 MW; EC32C271C982D47B CRC64;
 Query Match 50.4%; Score 989; DB 1; Length 377;
 Best Local Similarity 55.1%; Pred. No. 2.3e-60;
 Matches 188; Conservative 51; Mismatches 96; Indels 6; Gaps 3;

OY 258 GIRONNANTGRRRLVLDDEKMEKRISRMFYIMFLFLMGPLYVACVYFARGPVVP 317
 DB 259 GIRPAGPGRRARLVLEEKTEKRLCKMFAITLLFLLMGPLYVASTYRLVPRGAVP 318
 OY 318 GGFRTAAVWMSFAQINPVCIFSNRELRCRSTLLYXCR 358
 DB 319 QAVLTASVMTFPAQINPVYCFLEFRELDCRACRPPCQ 359
 RESULT 8
 GPRS_MOUSE STANDARD; PRT; 379. AA.
 ID GPRS_MOUSE
 AC 054897;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Probable G protein-coupled receptor GPR27 (Super conserved receptor
 GN expressed in brain 1).
 GN GPR27 OR SREB1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98140132; PubMed=9479505;
 RA O'Dowd B.F., Nguyen T., Marchese A., Cheng R., Lynch K.R.,
 RA Heng H.H.O., Kolakowski L.F. Jr., George S.R.;
 RT "Discovery of three novel G-protein-coupled receptor genes".
 RL Genomics 47:310-313(1998).
 CC -1- FUNCTION: ORPHAN RECEPTOR. POSSIBLE CANDIDATE FOR AMINE-LIKE G-
 CC PROTEIN COUPLED RECEPTOR (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (by similarity).
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC -----
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 CC -----
 CC EMBL; AF027955; AAC3540.1;
 CC MGD; MG1:1202299; Gpr27.
 DR InterPro: IPR000276; GPCR_Rhodpsn.
 DR Pfam: PF00001; 7tm.1; 1.
 DR PROSITE: PS00237; G_PROTEIN_RECPT_FL_1; FALSE_NEG.
 DR PROSITE: PS50262; G_PROTEIN_RECPT_FL_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;
 KW Multigene family.
 FT DOMAIN 1 26
 FT TRANSMEM 27 47
 FT DOMAIN 48 58
 FT TRANSMEM 59 79
 FT DOMAIN 80 100
 FT TRANSMEM 101 121
 FT DOMAIN 122 142
 FT TRANSMEM 143 163
 FT DOMAIN 164 185
 FT TRANSMEM 186 206
 FT DOMAIN 207 289
 FT TRANSMEM 290 310
 FT DOMAIN 311 324
 FT TRANSMEM 325 345
 FT DOMAIN 346 379
 FT DISULFID 98 175
 FT CARBOHYD 3 3
 SQ SEQUENCE 379 AA; 40036 MW; 9DAE96D2857E30D9 CRC64;
 Query Match 50.4%; Score 989; DB 1; Length 379;

DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PS00237; GPCR_RHODOPSIN.
DR PROSITE: PS00237; G-PROTEIN_RECEP_FL_1; 1.
DR PROSITE: PS00262; G-PROTEIN_RECEP_FL_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Lipoprotein; Palmitate.
FT DOMAIN 1 64
FT TRANSMEM 65 94
FT DOMAIN 95 104
FT TRANSMEM 105 131
FT TRANSMEM 132 142
FT TRANSMEM 143 164
FT DOMAIN 165 184
FT TRANSMEM 185 205
FT DOMAIN 206 237
FT TRANSMEM 238 261
FT DOMAIN 262 343
FT TRANSMEM 344 364
FT DOMAIN 365 379
FT TRANSMEM 380 403
FT DOMAIN 404 453
FT DISULFD 141 223
FT LIPID 401 401
FT CARBOHD 9 9
FT CARBOHD 22 22
FT CARBOHD 30 30
FT CARBOHD 35 35
FT CARBOHD 39 39
FT CARBOHD 39 39
FT SEQUENCE 453 AA; 51157 MW; 06217927B7482678 CRC64;
Query Match 13.1%; Score 257.5; DB 1; Length 453;
Best Local Similarity 24.2%; Pred No. 7.9e-11;
Matches 92; Conservative 65; Mismatches 164; Indels 59; Gaps 11
QY 16 SPFLAFLKLSGLGFIGVSVGNLLISILVYDKTLHRAVYFLDLCCSDILRSNACPP 75
Db 64 SDLMNLWRLVMSVIFELLSVFCNGLITLITLVNKKRLRTTNSFLSLASDLMLVNLKMP 123
QY 76 FVF--NSVRKNGSTWYTGILTCVIAFLVGLSCFHFAFMFLCSVTRYLAIAH---HREPT 130
Db 124 FTLLPNLMEN---FLIEGVCIRAAAYFEMGLSVSVSTFNVAISIERYSAINCPDKSRWQ 180
QY 131 KRLFWCTLCAYICWMTLSVAMAFPPVLDVGYVSILREE---DCTPGRSFRANDISG 186
Db 181 TRSNAY---RIYAAFTWVLSSTIMIDYLVNKKVTIPKMDRRVGHCCRLWMPKQVOOA-W 236
QY 187 FMLLALILATQLVYLKLIFFVHDKRRKKPQVFAAASQNTFNGPGASGQAANWMLAG 246
Db 237 YVLLITLIFELIPGVMI-VANGLSIRELYRGQFEMDKNEKAKIKNGVS----- 285
QY 247 FGRGCTPPTL-----LGIROMANTTGRRLLVIDEFKME-----KR 282
Db 286 -----TPRTIISGDEGDCYIQVTRRRNTMEMSTLTPSCYKMDRARINNSEAKIMAKR 340
QY 283 ISRMFYITFLFLIMGYLIACVARYV---ARGVYVGGFLTAIVMMSFQAAGINPFC 339
Db 341 VIRMLIVYVAMEFFICMADIEVANTKAFKDELASFTLTLGAPISFTHLSTYSACVNPITY 400
QY 340 IFSNRELRCFSTTLVLCRK 359
Db 401 CFMKKRFKAPFLGTFSSCIK 420
RESULT 10
GREL BALAM STANDARD; PRT; 476 AA.
AC 093126; 093128;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Probable G protein-coupled receptor NO9.

OS Balanus amphitrite (Barnacle).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Maxillopoda; Cirripedia;
OC Thoracica; Sessilia; Balanomorpha; Balanoidae; Balanidae; Balanus.
OX NCBI_TaxID=32267;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=DARWIN; PubMed=8917082;
RX MEDLINE=97074655; PubMed=8917082;
RA Isoal A., Kawahara H., Okazaki Y., Shizuri Y.;
RA "Molecular cloning of a new member of the putative G protein-coupled
RT receptor gene from barnacle Balanus amphitrite.";
RT Gene 175:95-100(1996)
CC - FUNCTION: ORPHAN G-PROTEIN COUPLED RECEPTOR.
CC - SUBCELLULAR LOCATION: Integral membrane protein (potential).
CC - SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC MOST SIMILAR TO ALPHA-2-ADRENERGIC RECEPTORS.
CC -----
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CC or send an email to license@sib.ch).

DR EMBL: D78363; BA01375.1;
DR EMBL: D78587; BA01424.1;
DR GCRDB: GCR_1153;
DR GCRDB: GCR_1154;
DR Interpro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm.1; 1.
DR PRINTS: PR00237; GPCR_Rhodopsn.
DR PROSITE: PS00237; G-PROTEIN RECEPTOR FL_1; 1.
DR PROSITE: PS50262; G-PROTEIN RECEPTOR FL_2; 1.
KM G-protein coupled receptor; Transmembrane; Glycoprotein.
FT DOMAIN 1 36
FT TRANSSEM 37 60
FT DOMAIN 61 69
FT TRANSSEM 70 93
FT DOMAIN 94 103
FT TRANSSEM 104 127
FT DOMAIN 128 152
FT TRANSSEM 153 172
FT DOMAIN 173 200
FT TRANSSEM 201 221
FT DOMAIN 222 375
FT TRANSSEM 376 396
FT DOMAIN 397 406
FT TRANSSEM 407 430
FT DOMAIN 431 476
FT SITE 113 113
FT SITE 208 208
FT SITE 208 208
FT CARBOHYD 13 13
FT CARBOHYD 17 17
FT DISULFID 106 192
FT CONFLICT 454 454
SO SEQUENCE 476 AA; 53245 MW; 0F55B51595D5CD06 CRC64;

Query Match 13.18; Score 257.5; DB 1; Length 476;
Best Local Similarity 21.68; Pred. No. 8.2e-11;
Matches 101; Conservative 60; Mismatches 173; Indels 133; Gaps 15;

QY 8 ADNLONLS-----PLTAF-----LKLTSIGFIISVSVGNLISILVKKTKLRAPRY 57
DB 11 ADVNTLVNSGCRPATLFWADHRLISLALFLNLVVAAGNLVMAVAVFSKLPVTNL 70
QY 58 FLIDLCSDIRSAICPEFVNSVNGSTWYGLTCKVIAFLVGLSCFHTAFMLFCISV 117
DB 71 FIVSLACADLVGMVLPF-SATLEVLDMVLXGDVWCWMLAVDMCMCSILNLCAISL 129

QY 118 TRYLAIAHREYTKRLTEWTCIAVICMWTLSVMAFPVLD----VGYTSFIREDQCT 173
DB 130 DRYLAVSOPISYPSLMSTRANOKLAAVWLSFVLCFEPPLVGMNDPRGTLSGSSACR 189
QY 174 F-----QHRSPRANSLGFMFLALILATOLVYLKLFVHDRRKMKPVQFAVAASQMW 228
DB 190 LTCELTENERGYIYTSALGSFPLPSYML-----FFGRIYRTAVSTTRALAQGF 238
QY 229 -----TFHGPASGOAAMNLA-- 245
DB 239 RTTKEDEGRLLRLIHGRSVYTORAQAAGARAHGQVRLTSEGCARONKPSFVHC 298
QY 246 -----GGR-----GPTPTLIG--IRON 262
DB 299 REDSRANKOYEITYTVGESRGRRRVPOPRPAKLISASQSEDSRPPRTISRVSRR 358
QY 263 ANTGRRRLVLDEPFMERKISRMFYIMFLTLGPIVACVWVFRG---PVPPG 319
DB 359 VHQARR-----FRMEKRAKTVGIYGLFILCHLPFFV-CY---LYRGFCADCVPL 407
QY 320 FLTAAVMSFAQGINPEVCIFSNRELRCFSTTL--LYCRSRRLPR 364
DB 408 LPSVFFMLGYCNSAVNCPVYALCSRDFRFAFSIICKCYCRGAMER 454

RESULT 11
5H2A_HUMAN
ID 5H2A_HUMAN STANDARD: PRT; 471 AA.
AC P28223;
DT 01-DEC-1992 (Rel. 24, Created)
DI 01-JUN-1994 (Rel. 29, Last sequence update)
DI 16-OCT-2001 (Rel. 40, Last annotation update)
DE 5-Hydroxytryptamine 2A receptor (5-HT_{2A}) (Serotonin receptor)
DE (5-HT-2)
GN HTR2A OR HTR2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain stem;
RX MEDLINE=92109767; PubMed=1722404;
RA Saltzman A.G., Morse B., Whitman M.M., Ivanschchenko Y., Jaye M.,
RA Felder S.;
RT "Cloning of the human serotonin 5-HT₂ and 5-HT_{2C} receptor subtypes.";
RN Biochem. Biophys. Res. Commun. 181:1469-1478(1991).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=92356792; PubMed=1323014;
RA Chen K., Yang W., Grimsby J., Shih J.C.;
RT "The human 5-HT₂ receptor is encoded by a multiple intron-exon gene.";
RN Brain Res. Mol. Brain Res. 14:20-26(1992).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=94308772; PubMed=8035173;
RA Cook E.H. Jr., Fletcher K.E., Walnwright M., Marks N., Yan S.Y.,
RA Leventhal B.L.;
RT "Primary structure of the human platelet serotonin 5-HT_{2A} receptor:
RT identify with frontal cortex serotonin 5-HT_{2A} receptor.";
RN J. Neurochem. 63:465-469(1994).
RN [4]
RP SEQUENCE OF 9-464 FROM N.A.
RC TISSUE=Brain;
RA Tritsch R.J., Robinson D.L., Sahagan B.G., Horlick R.A.;
RN submitted (xxx-1992) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE OF 105-218 FROM N.A.
RX MEDLINE=93049882; PubMed=1330647;
RA Stein N.J., van Huizen F., van Alebeek C., Brands J., Dijkema R.,
RA Tommaer J.A., Olijve W.;
RT "Genomic organization, coding sequence and functional expression of
RT human 5-HT₂ and 5-HT_{1A} receptor genes.";

FT	DISULFID	148	227		BY SIMILARITY.
FT	VARIANT	25	25	T -> N.	
FT	VARIANT	452	452	/FTID=VAR_003448.	
FT				H -> Y.	
FT				/FTID=VAR_003449.	
SQ	SEQUENCE	471 AA;	52603 MW;	EPRACOCBEC5379DA2 CRC64;	

Query Match 12.9%; Score 253.5; DB 1; Length 471;
Best Local Similarity 24.8%; Pred. No. 1.5e-10;
Matches 84; Conservative 61; Mismatches 147; Indels 47; Gaps 11

OY	30	IIGSVGVGNLISITLVKDKTLHRRPYFLDLCCSDIIRSAICPEPVFNYSKNSTWTY	89
Dd	84	VILLTLAGNIIIVIMAVSELEKQLQNATNFTEMSLAADMLGLTMPVSMLTIIYGWPL	143
OY	90	GLLTCKVIAFGVLSCFHAFMLPCGISRYRLAIA----HHRFYKRLLFWTCLAVICY	145
Dd	144	PSKLCAVMITLDVLTSTASIMHLCAISIDRYVAIONPPIHSHSFNSRTRKFAIKIA---V	199
OY	146	WTLSSAAFP--PLLVGYYSFIREDDOCPQRSPRANDSLCEFMILLALITLATOLVLYK	204
Dd	200	WTISGISMPIPEVLGLODDSKFKRGSGCL-----ADDN--FVLGSVVSFFPLTIWY	251
OY	205	LIFEVHDRKKMKPVQVFVAVSONMTTFHGPGASGOAAANWLAFGRGPPTPLGI-----	259
Dd	252	ITYFL---TKISLKKEATLC-----VSDLGTRAKLASFSF--LPQSSLSEKLFQ	296
OY	260	---RONANTTGRRLLVLDEFKMEKRISRMYIMTFELTLMGYPLVACYWRVPAR---	312
Dd	297	RSIHREPSYSTGR---TMOSISNIOCKACKVGIYFEFLFVVMWCPEFITINIMAVICKESC	353
OY	313	GPVVGGFLLTAWMSPAQAGINPVCIFSNELRCFS	351
Dd	354	NEDVIGALLNVFWIGLTSAAVNPLVTLENTYSAFS	392

RESULT 12		
ID	5H2A_MACMU	
AC	P50128.	STANDARD: PRT: 471 AA.
DT	01-OCT-1996 (Rel. 34, Created)	
DT	01-OCT-1996 (Rel. 34, Last sequence update)	
DT	01-OCT-1996 (Rel. 34, Last annotation update)	
DE	5-hydroxytryptamine 2A receptor (5-HT-2A) (Serotonin receptor)	
DE	(5-HT-2).	
GN	HT2A.	
OS	Macaque mulatta (Rhesus macaque).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Euhetia; Primates; Catarrhini; Cercopithecoidea;	
OC	Cercopithecinae; Macaca.	
OX	NCBI_Taxid-9544;	
RX	[1]	
RP	SEQUENCE FROM N.A.	
RX	JMJDINE-95315240; PubMed-7794950;	
RA	Johnson M.P., Baez M., Kursar J.D., Nelson D.L.;	
RT	"Species differences in 5-HT2A receptors: cloned pig and rhesus monkey 5-HT2A receptors reveal conserved transmembrane homology to the human rather than rat sequence";	
RT	Biochim. Biophys. Acta 1236:201-206(1995).	
CC	-1- FUNCTION: THIS IS ONE OF THE SEVERAL DIFFERENT RECEPTORS FOR 5-HYDROXYTRYPTAMINE (SEROTONIN). A BIOGENIC HORMONE THAT FUNCTIONS AS A NEUROTANSITTER, A HORMONE, AND A MITOGEN. THIS RECEPTOR MEDIATES ITS ACTION BY ASSOCIATION WITH G PROTEINS THAT ACTIVATE A PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER SYSTEM. THIS RECEPTOR IS INVOLVED IN TRACHEAL SMOOTH MUSCLE CONTRACTION, BRONCHCONSTRUCTION, AND CONTROL OF ALDOSTERONE PRODUCTION.	
CC	-1- SUBCELLULAR LOCATION: Integral membrane protein.	
CC	-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS. STRONGEST TO THE OTHER SHT-2 SUBTYPE RECEPTORS.	
CC	THIS SWISS-PROT ENTRY IS COPYRIGHT. IT IS PRODUCED THROUGH A COLLABORATION BETWEEN THE SWISS INSTITUTE OF BIOINFORMATICS AND THE EMBL OUTSTATION -	

RESULT	14
OPN3_MOUSE	
ID	OPN3_MOUSE
AC	09WUX7;
DT	16-OCT-2001 (Rel. 40, Created)
DT	16-OCT-2001 (Rel. 40, Last sequence update)
DE	16-OCT-2001 (Rel. 40, Last annotation update)
DE	Opsin 3 (Encephalopsin) (Panopsin).
GN	OPN3 OR ECPN.
OS	Mus musculus (Mouse).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX	NCBI_TaxID=10090;
RN	[1]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=9925248; Pubmed=1023400;
RA	Blackshaw S., Snyder S.H.;
RT	"Encephalopsin: a novel mammalian extraretinal opsin discretely
RT	localized in the brain.";
RL	J. Neurosci. 19:3681-3690(1999).
CC	- FUNCTION: May play a role in encephalic photoreception.
CC	- SUBCELLULAR LOCATION: Integral membrane protein.
CC	- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC	OPSN SUBFAMILY.
CC	-----
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration
CC	between the Swiss Institute of Bioinformatics and the EMBL Outstation
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CC	use by non-profit institutions as long as its content is in no way
CC	modified and this statement is not removed. Usage by and for commercial
CC	entities requires a license agreement (See http://www.isb.ch/announce/
CC	or send an email to license@isb-sib.ch).
CC	-----
DR	EMBL; AF140241; AAD32670.1; .
DR	MGD; MG11338022; Opn3.
DR	InterPro; IPR000276; GPCR_Rhodopsn.
DR	Pfam; PF00001; 7tm_1; 1.
DR	PRINTS; PR00237; GPCRHRDOPSN.
DR	PROSITE; PS00237; G-PROTEIN_RECP_F1_1; 1.
DR	PROSITE; PS00263; G-PROTEIN_RECP_F1_2; 1.
DR	PROSITE; PS00238; OPSIN; 1.
KW	Photoreceptor; Retinal protein; Transmembrane; Lipoprotein; Palmitate;
KW	G-protein coupled receptor.
FT	DOMAIN 1 38
FT	DOMAIN 39 63
FT	TRANSMEM 39 63
FT	DOMAIN 64 75
FT	EXTRACELLULAR (POTENTIAL).
FT	1 (POTENTIAL).
FT	CYTOPLASMIC (POTENTIAL).

Db	31	APLFSPITVERIALLLGLGALLGVLGNNLLVLLYKSPFLRPTHLFTVNLISGLDVLVS	90
Oy	72	ICFPVFNVS-YKNGSTWTVYGLTCKVIAFLVGLSGCFHNAFMFCISVTRYLIAIAHHREPT	130
Db	91	FGVITTFMSCLENG--WMDAVGACAMDGSGSGLEGFVSTLTTLTVAIYETIYVIVARV--	146
Oy	131	KRLFWTCLAVICMWTLVSMAAFPPVLDVGYFSFIREDOCTFOHRSERANDSIFMLL	190
Db	147	--INFSMAMRAITTYITWLXSLMAGAPFLGGNNRYIIDHGLGCTVWMRSNDANDS-SFVLE	203
Oy	191	LALILLAAQOLVYIKLIFVYHDKRRKKPQVFAVAASQNNTFHGPFGASGQAANMLAGFGRG	250
Db	204	LFGLGLVY-----PYGIIA-----HCYG-----	221
Oy	251	PTPPLILIRONANTGRRRLIVLDEPFMEKRISPMFIMPLFELTLMGPYLVCYWRWF	310
Db	222	---HLTYSVRLRCVEDJOTIOTIVITMLYERKKVAMCMLAFVFLTCMMPYITVTFELVYN	278
Oy	311	ARGPVVPGGFLTAAYVWMSFAQAGINPFVCIESNRELRL-----CFSTLLYCRK	359
Db	279	GYGHLVTFVTVSIVSYLFAKSSVTVPYIVITFEMNRKFRSRSLQLLGF--RLLRQCR	331
RESULT	15		
ALAA_ORYLA			
ALAA_ORYLA	STANDARD;	PRT;	470 AA.
AC	Q91175;		
DT	01-NOV-1997 (Rel. 35, Created)		
DT	01-NOV-1997 (Rel. 35, Last sequence update)		
DT	01-NOV-1997 (Rel. 35, Last annotation update)		
DE	Alpha-1A adrenergic receptor (MAR1).		
OS	Oryzias latipes (Medaka fish).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;		
OC	Acanthomorpha; Acanthopterygii; Percormorpha; Atherinomorpha;		
OC	Belontiiformes; Adrianchthyidae; Oryziinae; Oryzias.		
OX	NCBI_TaxID=8090;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=96184522; PubMed=8654394;		
RA	Yasuoaka A., Abe K., Arai S., Emoti Y.;		
RT	"Molecular cloning and functional expression of the		
RT	Alpha-1A-adrenoceptor of medaka fish, Oryzias latipes."		
RL	Eur. J. Biochem. 235:501-507(1996).		
CC	-!- FUNCTION: THIS ALPHA-ADRENERGIC RECEPTOR MEDIATES ITS ACTION BY		
CC	ASSOCIATION WITH G PROTEINS THAT ACTIVATE A PHOSPHATIDYLINOSITOL-		
CC	CALCIUM SECOND MESSENGER SYSTEM (BY SIMILARITY).		

QY 90 GTLCKVIAFLVGLSCFHTAFMLFCISTRYLAIA-----HHRFTKRLTFMTCLAVICMV 145
 DB 144 PSKCAWVIYLDVIFSTASIMILCALISDRYVALIONPIHNSFNSTKFLKIA-----V 199
 QY 146 WFLSVAMAF-PVLGVGYTSFTRFEDQCTFQHRSPRANSLGFMILLALILATQIVLK 204
 DB 200 WTISGVGMPPIPVFGLDDSKVFKQSGCLL-----ADNN--FVLIGSVAFEFPIITIMV 251
 QY 205 LIEFPHDRKKPKPVGFVAASQNMWFHFGASGQAANMLAGFGRGPTPELTIGI----- 259
 DB 252 ITYFL-----TIKSLCKEATLC-----VSDLSTRAKLAFSFS--LPQSSLSSEKLFQ 296
 QY 260 ----RONANTGRRRLVLDDEFKMEKRISRMFYIMTFLFTLMGPYLVACYWRFAR--- 312
 DB 297 RSIHPEPSYIGR---TMOSSINQORACKVIGIVFELFVVMCPEFINIMAVICKESC 353
 QY 313 GPVVGGLTAAVWMSFAOAGINPVCIFSNRELRCSTLLYC--RKSRLP 363
 DB 354 NEHVIGALLNFWGIVGLSSAVNPVLTLEFNKYSASF--RYIOCCQYKENRFP 405
 RESULT 2
 ID Q92492 PRELIMINARY; PRT; 396 AA.
 AC Q92492;
 DT 01-FEB-1997 (TREMblrel. 02, Created)
 DT 01-FEB-1997 (TREMblrel. 02, Last sequence update)
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
 DE CHOLECYSTOKININ-B RECEPTOR/GASTRIN RECEPTOR (CCR-B GASTRIN RECEPTOR ISOFORM) (FRAGMENT).
 GN CCKBR OR CCK-B.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OC NCBI_TaxID=9606;
 OX [1]
 RN RN SEQUENCE FROM N.A.
 RP TISSUE-LUNG;
 RC MEDLINE=93352657; PubMed=8349705;
 RA Ito M., Matsui T., Taniguchi T., Tsukamoto T., Murayama T., Arima N., Nakata H., Chiba T., Chihara K.;
 RT "Functional characterization of a human brain cholecystokinin-B receptor. A trophic effect of cholecystokinin and gastrin.";
 RL J. Biol. Chem. 268:18300-18305(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE-LUNG;
 RA MEDLINE=94038108; PubMed=8222757;
 RA Zimonjic D.B., Popescu N.C., Matsui T., Ito M., Chihara K.;
 RT "Localization of the human cholecystokinin-B/gastrin receptor gene (CCKBR) to chromosome 11p15.5--p15.4 by fluorescence in situ hybridization.";
 RL Cytogenet. Cell Genet. 65:184-185(1994).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE-LUNG;
 RA MEDLINE=95151633; PubMed=7848914;
 RA Ito M., Iwata N., Taniguchi T., Murayama T., Chihara K., Matsui T.;
 RT "Functional characterization of two cholecystokinin-B/gastrin receptor isoforms: a preferential splice donor site in the human receptor gene.";
 RL Cell Growth Differ. 5:1127-1135(1994).
 RN [4]
 RP SEQUENCE OF 16-26 FROM N.A.
 RA MEDLINE=95194412; PubMed=7887934;
 RA Miyake A.;
 RT "A truncated isoform of human CCK-B/gastrin receptor generated by alternative usage of a novel exon.";
 RL Biochem. Biophys. Res. Commun. 208:230-237(1995).
 DR EMBL; D21219; BA04759.1;
 DR EMBL; S76072; AA833740.1;
 DR HSSP; P02699; 1F88.

DR InterPro; IPR000276; GPCR_Rhodopsn.
 DR Pfam; PF00001; 7tm_1.1.
 DR PRINTS; PR00237; GPCR_RHODOPSIN.
 DR PROSITE; PS00237; G_PROTEIN_RECP_FL_1; UNKNOWN_1.
 DR PROSITE; PS00262; G_PROTEIN_RECP_FL_2; 1.
 FT NON_TER 396 396
 SQ SEQUENCE 396 AA; 43252 MW; A25D597CA903C0 CRC64;

Query Match 12.6%; Score 247.5; DB 4; Length 396;
 Best Local Similarity 24.7%; Pred. No. 9 6e-16;
 Matches 101; Conservative 48; Mismatches 145; Indels 115; Gaps 16;

QY 22 LKTSGLFIIGSVGNLLSILVYKDLHRAFYELDLCCSDILRSALCEPPEVNSV 81
 DB 5 IRTLVAVIFMISVGNMILITVGLSRRLRTVNAFLSLAVSDLLAVACMPEFTLLPN 64
 QY 82 KNGSTWYTGTLCKVIAFLVGLSCFHTAFMLFCISTRYLAIAHHRFTKRLTFWT----- 137
 DB 65 LMG-TFIFGVICKAVSYLGVSVSTLSLVAIALERSAICR-----PLQARVWQTRSH 119
 QY 138 CLAVICMWTLSVAMAF-PVLGVGYTSFTRFEDQCTFQHRSPRANSLGFMILL 192
 DB 120 AARVIVATMLSLGLMVPYV-----YTVQPVGPVYLQCVHMKPSARVQTSVLLLL 174
 QY 193 LIL-----LATQVYLKLIIF-----FVHRRKKRPQYFV 221
 DB 175 LEFTPGVMAVAAGLSRELTLGLRFGDSQSDSVNRNQGGLPQAVHNGRCRPE--T 232
 QY 222 AAYSON-----WTFHGPASGQAANMLAGFGCGPPTLLIGTRON 262
 DB 233 GAVGEDSDGCVYOLPRSPALLETALTAPPGS-----GSRPTQAKLA--- 276
 QY 263 ANTTGRRRLVLDDEFKMEKRISRMFYIMTFLFTLMGPYLVACYWRFARGP-----VVP 318
 DB 277 -----KKVVRMLVIVVFLFLCMLPVYSANTWRP-DGPGHRLSG 318
 QY 319 GFLTAAVWMSFAOAGINPVCIFSNRELRC-STSTLLYCKRSRLPREP 366
 DB 319 APSFIHLISYASACVNPVLYCCFMHRRFQACLETQARCC-----PRP 362
 RESULT 3
 ID Q16144 PRELIMINARY; PRT; 447 AA.
 AC Q16144;
 DT 01-NOV-1996 (TREMblrel. 01, Created)
 DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
 DE CHOLECYSTOKININ B RECEPTOR.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OC NCBI_TaxID=9606;
 OX [1]
 RN RN SEQUENCE FROM N.A.
 RP TISSUE-BRAIN;
 RC MEDLINE=94241526; PubMed=8185170;
 RA Herget T., Selth T., Wu S.V., Walsh J.H., Rozengurt E.;
 RT "Cholecystokinin stimulates Ca2+ mobilization and clonal growth in small cell lung cancer through CCKA and CCKB/gastrin receptors.";
 RL Ann. N. Y. Acad. Sci. 713:283-297(1994).
 DR EMBL; S70057; AA830766.2;
 DR HSSP; P02699; 1F88.
 DR InterPro; IPR000276; GPCR_Rhodopsn.
 DR Pfam; PF00001; 7tm_1.1.
 DR PRINTS; PR00237; GPCR_RHODOPSIN.
 DR PROSITE; PS00237; G_PROTEIN_RECP_FL_1; UNKNOWN_1.
 DR PROSITE; PS00262; G_PROTEIN_RECP_FL_2; 1.
 KW Receptor.
 SQ SEQUENCE 447 AA; 48418 MW; E3DAAE5BE1F0FB99 CRC64;

Query Match 12.6%; Score 246.5; DB 4; Length 447;
 Best Local Similarity 24.7%; Pred. No. 1.4e-15;
 Matches 101; Conservative 48; Mismatches 145; Indels 115; Gaps 16;

QY 22 LKLSIGFIIGSVGNLISILVYKDKTHRAPYFLDLCCSDIIRSAICPFVNSV 81
 DB 56 IRTTAVVIFLMSVGNMILIVLGLSRRLRTVNAFLSLAVSDLLAAVACMPFTLPN 115
 QY 82 KNGSTWYGLNCKVIAFLGLSCPHAFMLFCISVTRTALAHHRRTYRTRFWT---- 137
 DB 116 LMG-FFIFSTVICKAVSYLMGVSVSSTSLVAIALERYSAICR----PLQARWQRRSH 170
 QY 138 CLAVICMWTLSSVAAFP-PVLDTGYSTFREED---OCTFHRSRANDSLGEMLLA 192
 DB 171 AARVIAVATMLSLMVPV-----YTVQVPGPRVLQCVHRRPSARVQTSVLLLL 225
 QY 193 LIL-----LATQVLYLKLIF-----FVHRRKKRPVQFV 221
 DB 226 LEFIPGVNAVAVGLISRELXLGLRFGDSDSDSQRVRNQGILPAGVHONGRCRPE--T 283
 QY 222 AAVSON-----WTFHGPASGGAANWLAGFGGCPFPPLLGIRON 262
 DB 284 GAVGKSDGCVYOLPSPRALLETALTAPGGS-----GSRPTQAKLA---- 327
 QY 263 AMTGRRLVLVDEFEKMERISRMFYIMTFLTMGPYLIVACYWRYFARGP---VYPG 318
 DB 328 -----KRVVAMLLIVYVFLCMLPVSANTWRAP-DGPGAHRLSG 369
 QY 319 GFLTAVMWSFAQAGINPVCIFPSNRELRR-CSTSTLLYCKRSRLPREP 366
 DB 370 AIFSIFHLSTYSACVNPVLYCGMHRFRQACLETARCC-----PRPP 413

RESULT 4
 Q96KH9 PRELIMINARY; PRT; 378 AA.
 AC 096KH9;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE 5-HYDROXYTRYPTAMINE4 RECEPTOR.
 GN HTR4.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-BRAIN (HIPPOCAMPUS);
 RA Villaro M.T., Domenech T., Palacios J.M., Mengod G.;
 RT "Cloning and characterization of multiple human 5-HT4 receptor
 variants including a novel variant that lacks the alternatively
 spliced C-terminal exon."
 RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AJ278981; CAC22250.1;
 KW Receptor.
 SQ SEQUENCE 378 AA; 42745 MW; E45038EF832270D CRC64;

Query Match 12.4%; Score 243.5; DB 4; Length 378;
 Best Local Similarity 22.7%; Pred. No. 2.2e-15;
 Matches 88; Conservative 64; Mismatches 152; Indels 83; Gaps 13;

QY 9 DNILQNTSPILTAFA-----LKLSIGFIIGSVGNLISILVYKDKTHLR-APYFLDL 61
 DB 2 DKLIDANVSEEGFSGVERKVVLLFTSLVIMALGNLWVAVCMQRDLRIKTNFYIVS 61
 QY 62 LCCSDIIRSAICPFV-VENSVKNGSTWYGLTCKVIAFLCVLSCFHTAFMLFCISVTRY 120
 DB 62 LAFADLLVSVLMPGALIEVD--IWIYGEVCLVTRTSDVLLTASIFHLCCISIDRY 119
 QY 121 LAI-AHHRFTYRKLTFEWTCLAVICMWTLSSVAAFPVL---DVGTSYSTRREDQCTFQ 175

DB 120 YALCCQPLVYNNKMTPLRIALMLGCGWVLPFISFLPIMOGNNIGIIDLI-----E 171
 QY 176 HRSEFRANDS-----LGMILLALLILALDQVLYLKLIFVHDKRKKMP 217
 DB 172 KRKNQNSNSTYCVFMWVKPYAITSVAFYIPFLIMLAVAYRIYVTAKEHAHQIOMQR 231
 QY 218 VQFAAASQNTWTFHGPASGGAANWLAGFGGCPFPPLTLLGIRONANTGRRRLVLDFE 277
 DB 232 A-----GASSESRL-----QSADQSHTRM----- 251
 QY 278 KMERISRMFYIMTFLTMGPYLIVACYWRYFARGPVGFLTAVMWSFAQAGINPF 337
 DB 252 RTEKRAKTLCTIIGCFCLCAAPFVTNIYDPEI-DYTVPGQVWTAFLMLGYINSGLNPF 310
 QY 338 VCIFSNNELRRCFSTLLYCKRSRLPR 364
 DB 311 LYAFNLKSFRRAP-LIILCCDDERYRR 336

RESULT 5
 Q96KIO PRELIMINARY; PRT; 387 AA.
 AC 096KIO;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE 5-HYDROXYTRYPTAMINE4 RECEPTOR.
 GN HTR4.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-BRAIN (HIPPOCAMPUS);
 RA Villaro M.T., Domenech T., Palacios J.M., Mengod G.;
 RT "Cloning and characterization of multiple human 5-HT4 receptor
 variants including a novel variant that lacks the alternatively
 spliced C-terminal exon."
 RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AJ278979; CAC22248.1;
 KW Receptor.
 SQ SEQUENCE 387 AA; 44109 MW; 43019BED75AC9D0F CRC64;

Query Match 12.4%; Score 243.5; DB 4; Length 387;
 Best Local Similarity 22.7%; Pred. No. 2.3e-15;
 Matches 88; Conservative 64; Mismatches 152; Indels 83; Gaps 13;

QY 9 DNILQNTSPILTAFA-----LKLSIGFIIGSVGNLISILVYKDKTHLR-APYFLDL 61
 DB 2 DKLIDANVSEEGFSGVERKVVLLFTSLVIMALGNLWVAVCMQRDLRIKTNFYIVS 61
 QY 62 LCCSDIIRSAICPFV-VENSVKNGSTWYGLTCKVIAFLCVLSCFHTAFMLFCISVTRY 120
 DB 62 LAFADLLVSVLMPGALIEVD--IWIYGEVCLVTRTSDVLLTASIFHLCCISIDRY 119
 QY 121 LAI-AHHRFTYRKLTFEWTCLAVICMWTLSSVAAFPVL---DVGTSYSTRREDQCTFQ 175
 DB 120 YALCCQPLVYNNKMTPLRIALMLGCGWVLPFISFLPIMOGNNIGIIDLI-----E 171
 QY 176 HRSEFRANDS-----LGMILLALLILALDQVLYLKLIFVHDKRKKMP 217
 DB 172 KRKNQNSNSTYCVFMWVKPYAITSVAFYIPFLIMLAVAYRIYVTAKEHAHQIOMQR 231
 QY 218 VQFAAASQNTWTFHGPASGGAANWLAGFGGCPFPPLTLLGIRONANTGRRRLVLDFE 277
 DB 232 A-----GASSESRL-----QSADQSHTRM----- 251
 QY 278 KMERISRMFYIMTFLTMGPYLIVACYWRYFARGPVGFLTAVMWSFAQAGINPF 337
 DB 252 RTEKRAKTLCTIIGCFCLCAAPFVTNIYDPEI-DYTVPGQVWTAFLMLGYINSGLNPF 310

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QY 338 VCIFSNRELRCFSTTLTYCRSLRP 364
DB 311 LYAFLNKSFERRAF-LIILCCDDERRR 336

RESULT 6
075824 PRELIMINARY; PRT; 396 AA.
ID 075824
AC 075824;
DT 01-NOV-1998 (Tremblrel. 08, Created)
DT 01-NOV-1998 (Tremblrel. 08, last sequence update)
DE 01-DEC-2001 (Tremblrel. 19, last annotation update)
DE GASTRIN\CHOLECYSTOKININ BRAIN RECEPTOR (FRAGMENT).
GN CCKBR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-99087707; PubMed-9872672;
RA O'Brian K.C., Ali S.Y., Meier H.U.G., Bepler G.;
RT "An 84-kilobase physical map and repeat polymorphisms of the
RT gastrin/cholecystokinin brain receptor region at the junction of
RT chromosome segments 11p15.4 and 15.5.";
RL EMBL; AF074029; AAC27510.1;
DR EMBL; AF074035; AAC27510.1; JOINED.
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm.1; 1.
DR PRINTS: PR00237; GPCR_RHODOPSIN.
DR PROSITE: PS00237; G_PROTEIN_RECP_FL1; UNKNOWN_1.
DR PROSITE: PS0262; G_PROTEIN_RECP_FL2; 1.
KW Receptor.
FT NON_TER
SQ SEQUENCE 396 AA; 43286 MW; 54BB9A8D0257C4E5 CRC64;

Query Match 12.3%; Score 240.5; DB 4; Length 396;
Best Local Similarity 24.2%; Pred. No. 4.5e-15;
Matches 99; Conservative 49; Mismatches 146; Indels 115; Gaps 16;

QY 22 LKTLGFIQSVGNLISILVYKDKTLHRAPIYFLDLCCSDILRSALCPPEVFNVS 81
DB 5 IRTLYAVFELMSVGNMILIVLGLSRRLRTVNAFLSMASDILLAVACMPFLLPN 64
QY 82 KNGSWTGTCLCKVIAELGVLSCEFTAFMLPCISTRYLIAHHRFYTKRLTFWT 137
DB 65 IMG-FFIFGTICKAVSYLMGVSYSVSLVAIALERSAICR---PLQARVQTRSH 119
QY 138 CLAVICMWTLSVAMAF-PVLVDVGYTSFIREED---OCTFOHRSFRANDSLGEMLLA 192
DB 120 AARVIAVATMLSLGLMVPFV-----YTVQPRGPRVLDQVHNPBARVQTSVLLIL 174
QY 193 LIL-----LATQVLVYKLIF-----FVHDRRRKMPQVQV 221
DB 175 LFFIGVVAVAAYGLISRELTYGLRFGDSDSDQSRVRNOGLPQAVHONGCRPE--T 232
QY 222 AAVSON-----WTFHGPAGSGQAAMNMLAGFGRGPRPPTLLGTRON 262
DB 233 GAVGEDSDGCVQLPRSPALLETALTAPGPGS-----GSRPQAKILA--- 276
QY 263 AWTGRRRLLVLDFFMKRISRMFYIMTFLFTLNGPYLVACYWRFVARGP---VVP 318
DB 277 -----KRRVARMILIVYVFLCMLPYLSANTWAF--DGPQAHRLSG 318
QY 319 GFLTAVMWSFAQAGINPVCIFSNELRR-CESTLLTYCRSLRP 366
DB 319 AFSITHLISYASACVNPVLYGCMHRRROACLETCAACC-----PRP 362
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QY 338 VCIFSNRELRCFSTTLTYCRSLRP 364
DB 311 LYAFLNKSFERRAF-LIILCCDDERRR 336

RESULT 8
077254 PRELIMINARY; PRT; 419 AA.
ID 077254
AC 077254;
DT 01-NOV-1998 (Tremblrel. 08, Created)
DT 01-NOV-1998 (Tremblrel. 08, last sequence update)
DE 01-DEC-2001 (Tremblrel. 19, last annotation update)
DE G-PROTEIN COUPLED RECEPTOR.
OS Boophilus microplus (Cattle tick).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;
OC Parasitiformes; Ixodida; Ixodidae; Boophilus.
OX NCBI_TaxID=6941;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=N-STRAIN; TISSUE=LARVA;

QY 27 LGEFIQSVGNLISILVYKDKTLHRAPIYFLDLCCSDILRSALCPPEVFNVS 86
DB 102 LAEFLITAAVAGNLLVITSVACNRLQVTNFTYNAVADLLSATVLPFATHEVLG-F 160
QY 87 WYGTTLCKVIAELGVLSCEFTAFMLPCISTRYLIAHHRFYTKRLTFWTCLAVICMW 146
DB 161 MARGARACDVAWADVCTCAISILCTISVRYVGRHSIKYPSIMTERRAAAILALWM 220
QY 147 TLSVAMAFPYLV-----DVGYTSFIREDOCTPOHRSFRANDSLGEMLLAILLAT 198
DB 221 AAVIAVSVGLLKEKPEPPDERECGITEEGYAVF-----SLCSFYLPMAVIV--- 270
QY 199 QLVYKLIFVHDKRKKPQVQVAAVSONMTFHGPGASGOAAMNMLAGFGRGPRPPTLLG 258
DB 271 -VMICRY--YVASTTRSLR--AGVARE-----RGKASEVYLRIHCGSSGTIDRG 317
QY 259 ---IRONANTTGRRL-LVLDFFMKRISRMFYIMTFLFTLNGPYLVACYWRFVARGP 314
DB 318 HGAMRSTKGTFRSSLSRLKFESEKKAKTALIAVGVFLCWFPPFF-----VPLG 372
QY 315 VVP-----GGFLTAVMWSFAQAGINPVCIFSNELRCFSTTL-LYCRSLRP 366
DB 373 LFPOLKPEGVFKVIFWLGYSNCVNPDIYPCSSREFKRAFLRLRCOCHHSRRRRRP 430

Query Match 12.1%; Score 238.5; DB 6; Length 571;
Best Local Similarity 24.3%; Pred. No. 1.1e-14;
Matches 89; Conservative 61; Mismatches 161; Indels 47; Gaps 12;

QY 27 LGEFIQSVGNLISILVYKDKTLHRAPIYFLDLCCSDILRSALCPPEVFNVS 86
DB 102 LAEFLITAAVAGNLLVITSVACNRLQVTNFTYNAVADLLSATVLPFATHEVLG-F 160
QY 87 WYGTTLCKVIAELGVLSCEFTAFMLPCISTRYLIAHHRFYTKRLTFWTCLAVICMW 146
DB 161 MARGARACDVAWADVCTCAISILCTISVRYVGRHSIKYPSIMTERRAAAILALWM 220
QY 147 TLSVAMAFPYLV-----DVGYTSFIREDOCTPOHRSFRANDSLGEMLLAILLAT 198
DB 221 AAVIAVSVGLLKEKPEPPDERECGITEEGYAVF-----SLCSFYLPMAVIV--- 270
QY 199 QLVYKLIFVHDKRKKPQVQVAAVSONMTFHGPGASGOAAMNMLAGFGRGPRPPTLLG 258
DB 271 -VMICRY--YVASTTRSLR--AGVARE-----RGKASEVYLRIHCGSSGTIDRG 317
QY 259 ---IRONANTTGRRL-LVLDFFMKRISRMFYIMTFLFTLNGPYLVACYWRFVARGP 314
DB 318 HGAMRSTKGTFRSSLSRLKFESEKKAKTALIAVGVFLCWFPPFF-----VPLG 372
QY 315 VVP-----GGFLTAVMWSFAQAGINPVCIFSNELRCFSTTL-LYCRSLRP 366
DB 373 LFPOLKPEGVFKVIFWLGYSNCVNPDIYPCSSREFKRAFLRLRCOCHHSRRRRRP 430
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Query Match	12.0%	Score 236.5	DB 5	Length 419
Best Local Similarity	23.5%	Pred No. 1.2e-14		
Matches 89	Conservative 60	Mismatches 162	Indels 67	Gaps 13

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QY      26 SGGFIVGVSNNLLISILVYDKTLHRAFYFLDLDCSDILRSALICPP-VENSXNG 84
Db      63 SLSEFTTFTVVGNNVLIVCSVENHRLPKYQVNEFLVALADLAVALLVMEFNAYSIM-- 120
QY      85 STWTGYTLCKVIALGVLSCEFTAFMELCISVTRFLAIAHHRFTYKRLTFMTCIAVICM 144
Db      121 GRWVGLHRCCELMLTCDVLACSTASILNICALMDRWALHDPITNYQKTLIRVLLSTFL 180
QY      145 VWTLSVMAAFPPVLDVGITYSFTREDDOCTFHRSFRANDSLGPMILLA---LILLATQ 199
Db      181 VVAVIALISVPLP-IGWMDMEQDEDT---PCRLTQETGVLTLSAGSGFEPIPLIMS 234
QY      200 LVYLLILIEFVHRRKKM-----PYQVVAVSQWMTFHGPAS----- 236
Db      235 IYLLTI--FLATRRKIRERANAANAAPSSATRCATCAATVHSSVALLDQ--RHPSSEETPP 289
QY      237 ----GQAAMNWLAGEGRGPTPTLLGIRGNANMTG-----RRLLVLDEFKMEKRI 283
Db      290 PQHROQTEN-----RPSLADTSVLEBNGARPPSKVYFTCWEERQRT---SLSEERRA 339
QY      284 SRMEYIMTFLETLTMGPYLVACVYWRVAFGAPVYPGGFLLTAVMMSFQAQINDFVYCISFN 343
Db      340 ARVLIDVGVGVFVCLMPFIEMVYTAACDHCVQSDRLVNFIMVLGVNSALNPVITVEN 399
QY      344 RELRCCESTLLCYCKRS 361
Db      400 TDFRAFRS--LLCGNR 415

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RESULT	ID	Q9DBV6	PRELIMINARY;	PRT:	436 AA.
09DBV6	AC	Q9DBV6;			
DT	01-JUN-2001	(TREMBLrel. 17, Created)			
DT	01-JUN-2001	(TREMBLrel. 17, Last sequence update)			
DT	01-DEC-2001	(TREMBLrel. 19, Last annotation update)			
DE	ADULT MALE LUNG CDNA, RIKEN FULL-LENGTH ENRICHED LIBRARY,				
DE	CLONE:1200012013, FULL INSERT SEQUENCE.				
GN	CCCRAR.				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
OX	NCBI_TaxID=10090;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=C57BL/6J; TISSUE=LUNG;				
RX	MEDLINE=21085660; Pubmed=11217851;				
RA	Kawai J., Shinaigawa A., Shibata K., Yoshino M., Itoh M., Ishi Y.,				
RA	Aekawa T., Hara A., Fukunishi Y., Konno H., Aachii J., Fukuda S.,				
RA	Aikawa K., Iwawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,				
RA	Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,				
RA	Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,				

RA Flischmann W., Gaasterland T., Gissi C., Ring B., Kochia H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schiraldi L.M., Strubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Bottelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamuya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombergs P.,
 RA Nordone P., Ring B., Ringwald N., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Sessa T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitlaker C., Wilming L.,
 RA Wyshna-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohlsunki S.,
 RA Hayashizaki Y.,
 RT "Functional annotation of a full-length mouse cDNA collection",
 RL Nature 409:685-690(2001).
 DR EMBL: AK004730; BAB23512.1; -
 DR HSSP; P02699; 1P88.
 DR MGD; MGI:99478; Cckar.
 DR InterPro; IPR000276; GPCR_Rhodopsn.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCRHHODPSN.
 DR PROSITE; PS00237; G-PROTEIN_RECEP_FL1; UNKNOWN_1.
 DR PROSITE; PS02623; G-PROTEIN_RECEP_FL2; 1.
 SO SEQUENCE 436 AA; 48446 MW; 43B4AD57F080E08A CRC64;

Query Match	12.0%;	Score 236.5;	DB 11;	Length 436;
Best Local Similarity	23.3%;	Pred. No. 1.2e-14;		
Matches	95;	Conservative	67;	Mismatches 171;
			Indels	75;
			Gaps	13;

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QY 9 DNILQNLSPLT-----AFKLSLSLFIIGSVAVGNLLI 43
Db 5 DSLMNSNINTPPCSLGLENETLFCLLDQPHPSKEMQSAQVILLYSFILSLVSGDTLYT 64
QY 44 LLYKDKTLHRAPIYFLLDCCSDILRSALICEP--VFNSVKNKSGTWYTGTLCKVIAFLG 101
Db 65 VLIRNKRMRATYTNIPILLSLAVSDMLCLCEMPENLIPNLKD--FIFGSAVCKTTHYEM 121
QY 102 VLSCHTNFMFLCISVTVTKYLAIAHHRFTKRLTEFT----CLAVICAWTSLVSANAPPV 157
Db 122 GTSVSVSFTFNVAISLEBYGAIC--RPLOSRY--WQTSKHALKVIAWCSLFTTINTPYR 177
QY 158 LDVGYSYFIREBDQ----CFEOHRSFRANDSLGFWLLALLIL-----AQVLVYIKI 206
Db 178 IYSNLVPTTKANNQJATNANCRFLPSDAMQOSHOYTLILLFLIPGVVAVYAGLLSLEI- 236
QY 207 FFVHDRRRKAPVOYFAAASQWTFHGPASGQAAANWLAGFG---RGCPPTLLIRONA 263
Db 237 ---YQIGIFDASQKSAEKRLSSGGGGGSSSSRYEDSDOCYLOKSRPRKLEQOLS 293
QY 264 NTYGRRL-----LYLDEFKMERKISRMEYIMTFELFLIMGLPYLVAICYRVF-- 310
Db 294 TSSSGGRINIRSSGSAANLI-----AKRRVYIMLIVIVLFEFLCWMPLFSANMARAYDT 348
QY 311 -ARGVYVVGGLFAAVMMSFADAGINPVVCLFSNRELRCSTLLYC 357
Db 349 VSAEKHLSGTPISTLLSTYSSCVNPLIYCFMKNRFLGPMATPPCC 396

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RESULT	10
Q9DBLO	
ID	Q9DBLO
AC	Q9DBLO; PRELIMINARY;
DT	01-JUN-2001 (TReMBLrel. 17, Created)
DT	01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DT	01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE	ADRENERGIC RECEPTOR, ALPHA 1B.
GN	ADRA1B.
OS	Mus musculus (Mouse)
OC	Eukaryota; Metazoa; Chordata; Cranialta; Vertebrata; Euteleostomi;
OC	Mammalia; Euteheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX	NCBI_TaxID=10090;
ON	[1]

RP SEQUENCE FROM N.A.
RC STRAIN-C57BL/6J; TISSUE=LIVER;
RX MEDLINE-21085660; PubMed-11217851;
RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
RA Izawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Schirml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilmink L.,
RA Wyszaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,
RA Hayashizaki Y.;
CC "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL: AK004891; BAB3647.1;
DR HSSP: P29274; 1MMH.
DR MGD: MGI:104774; Adrb1.
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCRHOPOPSN.
DR PROSITE: PS00237; G_PROTEIN_RECEP_FL_1; 1.
DR PROSITE: PS00262; G_PROTEIN_RECEP_FL_2; 1.
DR KW G-protein coupled receptor; Glycoprotein; Transmembrane.
SQ SEQUENCE 515 AA; 56497 MW; 69D24E9978F81C1 CRC64;

Query Match 12.0%; Score 235.5; DB 11; Length 515;
Best Local Similarity 21.7%; Pred. No. 1.9e-14;
Matches 85; Conservative 65; Mismatches 173; Indels 69; Gaps 11;

QY 2 ANYSHADNLQNLSPITAFKLTSGFTIGV---SVGNLISILYKDKTHRAPY 57
DB 23 ANFTGNQTSNSTLPQDVTATRAISVGLVGAFLFAIVNITVLSVACNRHLRPTNY 82
QY 58 FLIDLCSDILRSACEPEFVNSKNGSTWYGLNCKVIAFLGLVSCPHAFMLFCISV 117
DB 83 FIVNLAIADLLSFTYVLPESATLEVIG-YVVLGRIFCDIMAAVDVLCCTISLSLAISI 141
QY 118 TRYLAHHRFYKRLFTWCLAVICWWTLSVMAAPVLDVGYSTFIREO-QCTFOH 176
DB 142 DRIGRYSIQYPLIVTRRAKAILALLSVWLSTYISIGPLL-GWKEPAPNDRECGVTE 199
QY 177 RSFRA-NDSCIG-FMLLALLLATQVYL-----KLIFVHDR 213
DB 200 EPPYALFSSISGYSIPLAVLIVMCRVYIAKRTTKMLEAGVMEKMSKSLTRIRISK- 258
QY 214 KMPVQFVAVSONMTHFGGASGQAANMLAGRGPTPTLLIGIONNTTGRRLV 273
DB 259 -----NHEDTLSTKA-----KGNPSSIAVR----- 282
QY 274 LDEFKMEKRISRMFYITFTFLMGVYLVACYWRVARGVVGGLTAAVMSFAOAG 333
DB 283 LEFESREKRAKAKTGLIVGFIILCMLPFIATLPGLSFTLKPRDAVKVYVWMLGYTNSC 342
QY 334 INPVCIFSNRELRCFSTTL-LYCRRSLPR 364
DB 343 LNPILYPCSSKEKRAKRAIRILGCGCCRRRR 374

RESULT 11
Q9CRR2 PRELIMINARY; PRT; 405 AA.

AC Q9CRR2;
DT 01-JUN-2001 (Trembl et al., 17, Created)
DT 01-JUN-2001 (Trembl et al., 17, Last sequence update)
DT 01-JUN-2001 (Trembl et al., 17, Last annotation update)
DE ADRENERGIC RECEPTOR, BETA 1 (FRAGMENT).
GN ADRA1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-C57BL/6J; TISSUE=EMBRYONIC LUNG;
RX MEDLINE-21085660; PubMed-11217851;
RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
RA Izawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Schirml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilmink L.,
RA Wyszaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,
RA Hayashizaki Y.;
CC "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL: AK018378; BAB31185.1;
DR MGD: MGI:87937; Adrb1.
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCRHOPOPSN.
DR PROSITE: PS00237; G_PROTEIN_RECEP_FL_1; 1.
DR PROSITE: PS00262; G_PROTEIN_RECEP_FL_2; 1.
DR KW G-protein coupled receptor; Glycoprotein; Transmembrane.
FT NON_TER 1
SQ SEQUENCE 405 AA; 44741 MW; 4F0F3FB956EF24 CRC64;

Query Match 11.9%; Score 234; DB 11; Length 405;
Best Local Similarity 24.6%; Pred. No. 2e-14;
Matches 89; Conservative 63; Mismatches 150; Indels 60; Gaps 16;

QY 27 LGFTIGSVGNLISILYKDKTHRAPYFLIDLCSDILRSACEPEFVNSKNGST 86
DB 4 LALIVLLVGNVAVIAVIAATPRLQTLNLFINSASADLVGLVVPFGATVWVG-R 62
QY 87 WTYGTCVKVIAFLVSCFTAFELFC-ISTRYLAIAHHRFYKRLFTWCLAVICV 145
DB 63 WEYSFCELTWSDVL-CVTAASITELCVIALDRILATSPRYOSLTTRARARLVCTV 121
QY 146 WTLGVMAFPVLDVGYSTFIREDO-----CTF-CHRSFR-ANDSIGMILLAL 193
DB 122 WAISALVSEFLPL---MHMRAESDEARCYNDPCDFVTRRAVAIASSVSVFVPLCI 178
QY 194 ILATQVLYLKLIFVHDRRRKPKYQFVAAYSONMTFPGASGQAANMLAGRGPT- 252
DB 179 M-----AFYLVF-----REAOKVKKIDSCER-----RFLGPARPSP 214
QY 253 -----PPTLLIGIONNTTGR--RLIVDEFKMEKRISRMFYITFTFLMGVYLV 303
DB 215 EPPSPGPPRADSLANRSSKRRSRRLVALREKALTLG-----INGVFLICMLPPL 270
QY 304 ACYWRVARGVVGGLTAAVMSFAOAGINPV-CIFSNRELRCFSTLLYCRKSL 362

Db 271 ANVKAHFR-DLVPRDLFEVFNMLGYANSAPNFIYC--RSPDRKAFQRLCCARRAC 327
 QY 363 PR 364
 Db 328 RR 329

RESULT 12

Q9GKAO PRELIMINARY; PRT; 414 AA.
 ID Q9GKAO;
 AC Q9GKAO;
 DT 01-MAR-2001 (Tremblrel. 16, Created)
 DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
 DE DOPAMINE D2 RECEPTOR SHORT ISOFORM.
 GN DRD2.
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OX NCBI_TaxID=9615;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20510028; PubMed=11054572;
 RA Myeong H., Jeoung D., Kim H., Ha J.H., Lee Y., Kim K.H., Park C.,
 RA Kaang B.,
 RT "Genomic analysis and functional expression of canine dopamine D2
 RT receptor."
 RL Gene 257:99-107(2000).
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 DR EMBL: AF293962; AAC34495.1;
 DR InterPro: IPR000276; GPCR_Rhodopsn.
 DR Pfam: PF00001; 7tm_1; 1.
 DR PRINTS: PR00237; GPCRHHODOPSN.
 DR PROSITE: PS00237; G-PROTEIN RECP.F1.1; 1.
 DR PROSITE: PS0262; G-PROTEIN RECP.F1.2; 1.
 KW G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane.
 SQ SEQUENCE 414 AA; 47289 MW; 7DAD2AD48621CD74 CRC64;

Query Match 11.9%; Score 234; DB 6; Length 414;
 Best Local Similarity 21.2%; Pred. No. 2e-14;

Matches 83; Conservative 70; Mismatches 163; Indels 76; Gaps 12;

QY 24 LPSLGIIGSVVGNLLISILVKKTLHRAPIYFLDLCCSDILRSALCFPEFVNSVKN 83
 Db 41 LTLIFIT---VFGNVLCMAVSREKALQTTNTNVLIVSLAVADLVATLVMPWVYLEV 97
 QY 84 GSTWYTGILTKVIAFLGVLSCHFTAFMLFCISVTRILAIHHRFYTKRLTFWTLAV-I 142
 Db 98 GE-WKFSRIHCDIFVTLDMVMTASILNLCASIDRYTAVAMPMLYNTRRSSKRRVTMI 156
 QY 143 CMWVTLVAMAFPPVLDVGYTSFIREDOCTFOHRSFRANDSLGFMILLALILATOLVY 202
 Db 157 AIVWVLSFTISCPILFGLNN---TDONECTIANPAFVYSSI---VSFYVPIVTLVLY 209
 QY 203 LKLIFFVHDRK-----MKPVQFAVAASQNM----- 228
 Db 210 IKIYIVLRRRRKRVNTERSSRAFRANLKAFLKEARAQLEMEMLSTSPERTRYSPI 269
 QY 229 -----TFHGPASGOAANWLAGFGGPTPTLLGI-----RONANT 265
 Db 270 PPSHQTLPLDPSSHGHGHTADSPAKPEKN-GHAKDHPKIAKIFEQSMNGKTRTSIKT 328
 QY 266 TGRRLVLVDEFMEKRISRMFYIMTFLFLTMGPYLVACWVRPAPVPVPGGLTAAY 325
 Db 329 MSRRKL-----SQEKKATOMALIVGVFIICLPFFTHILNHCECN-IPVLYSAFT 383
 QY 326 WMSFAQAGINPFCIFSNRELRCFSTLLYC 357
 Db 384 WLGYVNSAVNPFIITYTFNIEFRKAF-LKILHC 414

RESULT 13

Q9GK99 PRELIMINARY; PRT; 414 AA.
 ID Q9GK99;
 AC Q9GK99;
 DT 01-MAR-2001 (Tremblrel. 16, Created)
 DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
 DE DOPAMINE D2 RECEPTOR SHORT ISOFORM.
 GN DRD2.
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OX NCBI_TaxID=9615;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20510028; PubMed=11054572;
 RA Myeong H., Jeoung D., Kim H., Ha J.H., Lee Y., Kim K.H., Park C.,
 RA Kaang B.,
 RT "Genomic analysis and functional expression of canine dopamine D2
 RT receptor."
 RL Gene 257:99-107(2000).
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 DR EMBL: AF293964; AAC34497.1;
 DR InterPro: IPR000276; GPCR_Rhodopsn.
 DR Pfam: PF00001; 7tm_1; 1.
 DR PRINTS: PR00237; GPCRHHODOPSN.
 DR PROSITE: PS00237; G-PROTEIN RECP.F1.1; 1.
 DR PROSITE: PS0262; G-PROTEIN RECP.F1.2; 1.
 KW G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane.
 SQ SEQUENCE 414 AA; 47288 MW; 4E330ADC400FCB5C CRC64;

Query Match 11.9%; Score 234; DB 6; Length 414;
 Best Local Similarity 21.2%; Pred. No. 2e-14;

Matches 83; Conservative 70; Mismatches 163; Indels 76; Gaps 12;

QY 24 LPSLGIIGSVVGNLLISILVKKTLHRAPIYFLDLCCSDILRSALCFPEFVNSVKN 83
 Db 41 LTLIFIT---VFGNVLCMAVSREKALQTTNTNVLIVSLAVADLVATLVMPWVYLEV 97
 QY 84 GSTWYTGILTKVIAFLGVLSCHFTAFMLFCISVTRILAIHHRFYTKRLTFWTLAV-I 142
 Db 98 GE-WKFSRIHCDIFVTLDMVMTASILNLCASIDRYTAVAMPMLYNTRRSSKRRVTMI 156
 QY 143 CMWVTLVAMAFPPVLDVGYTSFIREDOCTFOHRSFRANDSLGFMILLALILATOLVY 202
 Db 157 AIVWVLSFTISCPILFGLNN---TDONECTIANPAFVYSSI---VSFYVPIVTLVLY 209
 QY 203 LKLIFFVHDRK-----MKPVQFAVAASQNM----- 228
 Db 210 IKIYIVLRRRRKRVNTERSSRAFRANLKAFLKEARAQLEMEMLSTSPERTRYSPI 269
 QY 229 -----TFHGPASGOAANWLAGFGGPTPTLLGI-----RONANT 265
 Db 270 PPSHQTLPLDPSSHGHGHTADSPAKPEKN-GHAKDHPKIAKIFEQSMNGKTRTSIKT 328
 QY 266 TGRRLVLVDEFMEKRISRMFYIMTFLFLTMGPYLVACWVRPAPVPVPGGLTAAY 325
 Db 329 MSRRKL-----SQEKKATOMALIVGVFIICLPFFTHILNHCECN-IPVLYSAFT 383
 QY 326 WMSFAQAGINPFCIFSNRELRCFSTLLYC 357
 Db 384 WLGYVNSAVNPFIITYTFNIEFRKAF-LKILHC 414

RESULT 14

Q96RE8 PRELIMINARY; PRT; 466 AA.
 ID Q96RE8;
 AC Q96RE8;
 DT 01-DEC-2001 (Tremblrel. 19, Created)
 DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)

DT 01-DEC-2001 (Tremblrel. 19, last annotation update)
 DE ADENERGIC RECEPTOR ALPHA-1A.
 GN ADRA1A.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Banerjee A.G.N., Artl A.;
 RT "RT-PCR cloning and sequence analysis of adrenergic receptor subtype-
 alpha-1a cDNA from human prostatic cell-line DU-145."
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF35806; AAK7717.1;
 KW Receptor.
 SQ SEQUENCE 466 AA; 51431 MW; 876CBFB3E32B7A1 CRC64;

Query Match 11.9%; Score 233.5; DB 4; Length 466;
 Best Local Similarity 23.3%; Pred. No. 2,6e-14;
 Matches 90; Conservative 65; Mismatches 149; Indels 83; Gaps 15;

QY 8 ADNLTONTSPLE---AFKLTSLGFLIGSVVGNLLISILVYDKTLHRAPIYFLDCC 64
 DB 11 SSNCQAPAPVVISKAILLGLVGLGILFVGNLIIIVSVACHRLHSVTHRYIVNLAV 70
 QY 65 SDLSAICFPF--VENSVMKNGSTWYGTLLCKVIAFLVLCGFHAFMFCISVTRYIA 122
 DB 71 ADLLTSLVLPESAIFEVY---GVNAFGHVPFCNMAVAVLCTASIMGLCISIDRYIG 127
 QY 123 IAHNFYTKRLTFWTCGLAVICMWTLSVMAFPVLDVGTYSFIREDOCTPHRSFRAN 182
 DB 128 VSHPRPTPTIVQRRGLMALCVMALSLVISIGPLEG---WRQPAEDDTICO---IN 179
 QY 183 DSLGFMALLA---ILLATOLVYLKLFVHDDR-----KMPVQFAVAVSON 227
 DB 180 EEPGVLVSALGSFLPLAIIIVMCRYVAVAKRESRGKSGIKTKSDQVTLIHKR 239
 QY 228 WTEHGP-GASGOAANWLAGFGRGPTPLLLGIROMANTTGRRLLVLEFKMEKRISRM 286
 DB 240 ---NAPAGSGGMAKAKTTHFS-----VRLT---KFSKKKAANT 273
 QY 287 FYIMFLELTLMGPYLVACYWRFVARGPVVPGGF-----LTAVMSFQAQGIN 335
 DB 274 LGIVGCEVLCWLPFEL-----VMPISGFEPPDERKSETVKIVFWGLYMSGIN 322
 QY 336 PFVCFISNRELRCFSTTL--LYCRK 359
 DB 323 PIIVCSOEFKKAQNVLRIOCLCRK 349

RESULT 15
 Q9N297 PRELIMINARY; PRT; 422 AA.
 AC Q9N297;
 DT 01-OCT-2000 (Tremblrel. 15, Created)
 DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
 DE SEROTONIN RECEPTOR 1A.
 GN HTR1A.
 OS Gorilla gorilla (gorilla).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Gorilla.
 OX NCBI_TaxID=9593;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA STRAIN-GORILLA-01;
 RA Kitano T., Kobayekawa H., Saitou N.;
 RT "Silver Project."
 RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 DR EMBL; AB041405; BAA94490.1;

DR HSSP; P29274; 1MMH.
 DR InterPro; IPR000276; GPCR_Rhoopsn.
 DR Pfam; PF00001; 7tm_1.1.
 DR PRINTS; PR00237; GPCRHHOOPS.
 DR PROSITE; PS00237; G_PROTEIN_RECPT_FL_1; 1.
 DR PROSITE; PS0262; G_PROTEIN_RECPT_FL_2; 1.
 KW G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane.
 SQ SEQUENCE 422 AA; 46154 MW; 012335E0403F1B90 CRC64;

Query Match 11.9%; Score 233; DB 6; Length 422;
 Best Local Similarity 20.9%; Pred. No. 2,6e-14;
 Matches 86; Conservative 72; Mismatches 170; Indels 84; Gaps 15;

QY 15 LSPLE-AFLKLTSLGFLIGSVVGNLLISILVYDKTLHRAPIYFLDCCSILIRSA 71
 DB 28 ISDVTSYQVITSLILGTLIFCAVGLACVAAVMAIALERSIONVANYLIGSLAVDLMVSY 87
 QY 72 ICFPF-----VENSVMKNGSTWYGTLLCKVIAFLVLCGFHAFMFCISVTRYIAAH 126
 DB 88 LVLPMAALYQVLRK-----WTLGOVYCDLFIALDVLCSTSLHLCAIALDRYMAITDP 141
 QY 127 RFYTKRLTFWTCGLAVICMWTLSVMAFPVLDVGTYSFIREDOCTPHRSFRANDSL 185
 DB 142 IDYVNRTPRAAALISITWLGFLISIPPLGKRTPEDSDPDACISKDHGTTITSTF 201
 QY 186 G-PMALLAILLATOLVYLKLFVHDDRKKMPVQFAVAVSONWTEHGP-----GASG 237
 DB 202 GAFYIPLLLMLVLYGRIFRAARPRI--RKTVMKVEKGTADTRHGAAPAPKKSVMGSG 259
 QY 238 QAANWLAGF-----GAGTPP-- 253
 DB 260 ---SRNRLGVESKAGALCANGAVROGDDGALEVEVHNVGNSKEHLPLPSEAGPPPCA 317
 QY 254 PTLGIROMANTTGRRLLVLEFKMEKRISRMFYIMFLELTLMGPYLVACYWRFVARG 313
 DB 318 PASFERKNERNAKAKRMALAREKTYKTG---LIMGFILLCWLPFYVALVLPCE 373
 QY 314 ---PVVPGFELTAAVWMSFQAQINPFVCFISNRELRCFSTTL--LYCRK 359
 DB 374 SCHMPTLGAIIIN---WLGYSNLSLNVIAVFNKDKQNAFKRIKCKFCQ 422

Search completed: July 19, 2002, 14:43:05
 Job time: 226 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 19, 2002, 14:33:24 ; Search time 32.06 Seconds
(without alignments)
1281.887 Million cell updates/sec

Title: US-09-698-419-14
Perfect score: 1963
Sequence: 1 MANYSHADNLTIONLSPLFA.....STLLYCKSRNLPREYCVI 370

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: A_Geneseq-032802:*
2: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1980.DAT:*
3: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1981.DAT:*
4: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1982.DAT:*
5: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1983.DAT:*
6: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1984.DAT:*
7: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1985.DAT:*
8: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1986.DAT:*
9: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1987.DAT:*
10: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1988.DAT:*
11: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1989.DAT:*
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19: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1997.DAT:*
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21: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1999.DAT:*
22: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA2000.DAT:*
23: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	1963	100.0	370	20	AA130533	A G protein-couple
2	1963	100.0	370	20	AA130537	A G protein-couple
3	1963	100.0	370	21	AA171303	Human orphan G pro
4	1963	100.0	370	21	AA1802837	Human G protein co
5	1963	100.0	370	21	AA1805145	Human G protein co
6	1963	100.0	370	21	AA154323	Amino acid sequenc
7	1963	100.0	370	21	AA173558	A G-protein couple
8	1963	100.0	370	22	AA173558	Human Gp27-like G
9	1963	100.0	379	22	AA1802497	Human Gp27-like G
10	1959	99.8	370	22	AA1802497	Human expressed po
11	1288.5	65.6	373	21	AA171300	Human RECAP polypro

Result No.	Score	Match	Length	DB	ID	Description
12	1288.5	65.6	373	21	AA1802834	Human G protein co
13	1283.5	65.4	373	20	AA130534	A G protein-couple
14	1283.5	65.4	373	22	AA197747	Human Koralisa pro
15	1283.5	65.4	378	22	AA199953	Human expressed po
16	1276.5	65.0	373	20	AA130538	A G protein-couple
17	1274.5	64.9	373	21	AA132237	Human 77M receptor
18	1270.5	64.7	373	21	AA199715	Human G-protein co
19	998.5	50.9	375	20	AA130532	A G protein-couple
20	998.5	50.9	375	21	AA171288	Human orphan G pro
21	998.5	50.9	375	21	AA180282	Human G protein co
22	989	50.4	377	20	AA130536	A G protein-couple
23	987	50.3	377	20	AA199947	Human expressed po
24	633	32.2	183	22	AA110284	Human expressed po
25	633	32.2	183	22	AA110284	Human CDNA SEQ ID
26	633	32.2	183	22	AA118119	Novel human uterin
27	633	32.2	183	22	AA118365	Human endocrine po
28	633	32.2	183	22	AA118672	Renal and cardova
29	633	32.2	183	22	AA121662	Novel human neopla
30	594.5	30.3	184	20	AA130813	Human secreted pro
31	577	29.4	144	22	AA199980	Human expressed po
32	577	29.4	144	22	AA110295	Human CDNA SEQ ID
33	577	29.4	144	22	AA118121	Novel human uterin
34	577	29.4	144	22	AA118374	Human endocrine po
35	577	29.4	144	22	AA118673	Renal and cardova
36	577	29.4	144	22	AA121667	Novel human neopla
37	522	26.6	100	22	AA111047	Human SREB2 homolo
38	473	24.1	180	22	AA199975	Human expressed po
39	473	24.1	180	22	AA110259	Human CDNA SEQ ID
40	473	24.1	180	22	AA118110	Novel human uterin
41	473	24.1	180	22	AA118352	Human endocrine po
42	473	24.1	180	22	AA118658	Renal and cardova
43	473	24.1	180	22	AA121652	Novel human neopla
44	470	23.9	143	22	AA180959	Human ngPCR55. Ho
45	388	19.8	124	22	AA105832	Human polypeptide

ALIGNMENTS

Result No.	Score	Match	Length	DB	ID	Description
1	1963	100.0	370	20	AA130533	A G protein-couple
2	1963	100.0	370	20	AA130537	A G protein-couple
3	1963	100.0	370	21	AA171303	Human orphan G pro
4	1963	100.0	370	21	AA1802837	Human G protein co
5	1963	100.0	370	21	AA1805145	Human G protein co
6	1963	100.0	370	21	AA154323	Amino acid sequenc
7	1963	100.0	370	21	AA173558	A G-protein couple
8	1963	100.0	370	22	AA173558	Human Gp27-like G
9	1963	100.0	379	22	AA1802497	Human Gp27-like G
10	1959	99.8	370	22	AA1802497	Human expressed po
11	1288.5	65.6	373	21	AA171300	Human RECAP polypro

PS Example 1; Page 53-54; 72pp; Japanese.

XX The present sequence represents a G protein-coupled receptor protein,
CC designated SREB2. The protein is expressed in the central nervous
CC system. The SREB2 products are used for the diagnosis and treatment
CC of diseases of the central nervous system, including inflammatory
CC disorders of immunological origin.

XX Sequence 370 AA:

Query Match 100.0%; Score 1963; DB 20; Length 370;

Best Local Similarity 100.0%; Pred. No. 2e-208; Mismatches 0; Indels 0; Gaps 0;

Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MANYSHADNITLONLSPLTAFLKLTSLGFIIGSVVGNLLISILVYKDTLHRAPIYFL 60
DB 1 manyshadnllqnlspaltakltslgfllgsvvgnllslllvkdtlhrapyfll 60
QY 61 DLCCSDILRSALCFPFVNSVKNSTWYGLTCKVIAFLGVLSCFHTAFMLFCISVTRY 120
DB dlccsdilrsalcfpfvnsvknstwyglctckviaflgvlscfhtafmlfcisvtry 120
QY 121 LAIAHHRFYTKRLFTWTCIAVICWMTLSVMAFPVLDVGYTSFIREDOCTFOHRSFR 180
DB lalahrftytkrlftwtclavicmwltsvmafpvldvgytsfiredoctfohrsfr 180
QY 181 ANDSLGFMILLALITATOLVYLKLIFFVHDKRKKPVOFVAASOMTFHGGASGOAA 240
DB andslgfmillalitalatolvylkliffvhdrrkmpvofvaasomtfhggasgaa 240
QY 241 ANMLAGRGPTPTLLGIRONANTGRRRLVLDDEFKMERISRMFYIMTFLTLMP 300
DB anmlagrgptptllgironantgrrrlvlddefkmerisrmfyimtfltlmp 300
QY 301 YLVACYRWVFARGPVPGFLLTAAMVMSFAOAGINPVCISNRELRCFSTLLYCRKS 360
DB ylvacyrwvfarpgvpvgflltaamvmsfaaginpvcisfnrelrcfstlllycrks 360
QY 361 RLPREPYCVI 370
DB 361 rlprepycvi 370

RESULT 2
ID AAY30537 standard; Protein: 370 AA.
AC AAY30537;
DT 15-NOV-1999 (first entry)
XX
DE A G protein-coupled receptor protein designated SREB2.
XX
KW G protein-coupled receptor protein; SREB2; central nervous system;
KW inflammatory disorder; immunological.
XX
OS Rattus sp.
XX
PN MO9946378-A1.
XX
PD 16-SEP-1999.
XX
PE 11-MAR-1999; 99WO-JP01191.
XX
PR 12-MAR-1998; 98JP-0060245.
PR 03-FEB-1999; 99JP-0026774.
XX
XX (YAMA) YAMANOUCHI PHARM CO LTD.
XX
PI Makumoto M, Sugimoto T, Takasaki J, Satto T, Kamohara M;
XX
DR WPI; 1999-551407/46.

DR N-PSDB: AA210577.

XX G protein-coupled receptor proteins expressed in the central nervous
PT system and genes encoding them

XX Example 4; Page 66-67; 72pp; Japanese.

PS The present sequence represents a G protein-coupled receptor protein,
CC designated SREB2. The protein is expressed in the central nervous
CC system. The SREB2 products are used for the diagnosis and treatment
CC of diseases of the central nervous system, including inflammatory
CC disorders of immunological origin.

XX Sequence 370 AA:

Query Match 100.0%; Score 1963; DB 20; Length 370;

Best Local Similarity 100.0%; Pred. No. 2e-208; Mismatches 0; Indels 0; Gaps 0;

Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MANYSHADNITLONLSPLTAFLKLTSLGFIIGSVVGNLLISILVYKDTLHRAPIYFL 60
DB 1 manyshadnllqnlspaltakltslgfllgsvvgnllslllvkdtlhrapyfll 60
QY 61 DLCCSDILRSALCFPFVNSVKNSTWYGLTCKVIAFLGVLSCFHTAFMLFCISVTRY 120
DB dlccsdilrsalcfpfvnsvknstwyglctckviaflgvlscfhtafmlfcisvtry 120
QY 121 LAIAHHRFYTKRLFTWTCIAVICWMTLSVMAFPVLDVGYTSFIREDOCTFOHRSFR 180
DB lalahrftytkrlftwtclavicmwltsvmafpvldvgytsfiredoctfohrsfr 180
QY 181 ANDSLGFMILLALITATOLVYLKLIFFVHDKRKKPVOFVAASOMTFHGGASGOAA 240
DB andslgfmillalitalatolvylkliffvhdrrkmpvofvaasomtfhggasgaa 240
QY 241 ANMLAGRGPTPTLLGIRONANTGRRRLVLDDEFKMERISRMFYIMTFLTLMP 300
DB anmlagrgptptllgironantgrrrlvlddefkmerisrmfyimtfltlmp 300
QY 301 YLVACYRWVFARGPVPGFLLTAAMVMSFAOAGINPVCISNRELRCFSTLLYCRKS 360
DB ylvacyrwvfarpgvpvgflltaamvmsfaaginpvcisfnrelrcfstlllycrks 360
QY 361 RLPREPYCVI 370
DB 361 rlprepycvi 370

RESULT 3
ID AAY71303 standard; Protein: 370 AA.
AC AAY71303;
DT 02-NOV-2000 (first entry)
XX
DE Human orphan G protein-coupled receptor hCHN3.
XX
KW Human; orphan G protein-coupled receptor; GPCR; hCHN3; drug screening;
KW transmembrane receptor; expressed sequence tag; EST; signal cascade.
XX
OS Homo sapiens.
XX
PN WO200031258-A2.
XX
PD 02-JUN-2000.
XX
PE 13-OCT-1999; 99WO-US23687.
XX
PR 20-NOV-1998; 98US-0109213.
PR 16-FEB-1999; 99US-0120416.
PR 26-FEB-1999; 99US-0121852.

XX	12-MAR-1999;	99US-0123946.
XX	PR 12-MAR-1999;	99US-0123949.
XX	PR 28-MAY-1999;	99US-0136436.
XX	PR 28-MAY-1999;	99US-0136437.
XX	PR 28-MAY-1999;	99US-0136439.
XX	PR 28-MAY-1999;	99US-0136567.
XX	PR 28-MAY-1999;	99US-0137127.
XX	PR 28-MAY-1999;	99US-0137131.
XX	PR 29-JUN-1999;	99US-0141448.
XX	PR 29-SEP-1999;	99US-0156555.
XX	PR 29-SEP-1999;	99US-0156633.
XX	PR 29-SEP-1999;	99US-0156634.
XX	PR 29-SEP-1999;	99US-0156653.
XX	PR 01-OCT-1999;	99US-0157280.
XX	PR 01-OCT-1999;	99US-0157281.
XX	PR 01-OCT-1999;	99US-0157282.
XX	PR 01-OCT-1999;	99US-0157293.
XX	PR 01-OCT-1999;	99US-0157294.
XX	PR 12-OCT-1999;	99US-0416760.
XX	PR 12-OCT-1999;	99US-0417044.
XX	(AREN-) ARENA PHARM INC.	
XX	PA	
XX	PI Chen R, Dang HT, Liao CW, Lin I;	
XX	DR WPI: 2000-400066/34.	
XX	DR N-PSDB: AAD01130.	
XX	PT Novel human orphan G protein-coupled receptors and the encoding cDNAs	
XX	PT for use in the identification of G protein-coupled receptor agonists -	
XX	Claim 50; Page 74-75; 102pp; English.	

	Query Match	100.0%;	Score 1963;	DB 21;	Length 370;
	Best Local Similarity	100.0%;	Pred. No. 2e-208;		
	Matches 370;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps
QY	1 MANTSHADNLONSPITAFILKLTSLGIFIGVSVGNLISILVYKDKTIRHAPYFL 60				
Db	1 manyshaadnllqhspltafikltslglfivsvgnllslilvdktlhrpyyfl 60				
QY	61 DLCCSDILRSALCEPEVNSVKNSTMTYGTGKVAFLGVLSCFPAFLFCISTRY 120				
Db	61 dlccsdilrsalcipfyfnsvknstwyglclckvafllgvsclfnatmlfcistry 120				
QY	121 LAIAHHRFYRLTFMFCIAVCVWMTLSVMAAPPVLDVGYSFIREDOCTFOHRSFR 180				
Db	121 laiahhrfytkrltfvcciaicmwvltswamaprpvldvgytsfiredoctfnhsfr 180				
QY	181 ANDSLGEMLLALILATQVLVYLKLFVHDDRKKRPQVFAAVSQQMTFHPGASGOAA 240				
Db	181 andslgfmllalilalqlyvylklffvhdrrkmpqgfaavsqmwfthpgasgaa 240				
QY	241 ANMLAGRGRTPTPLIGIRONANTTGRRLVLVDERMEKRISRIMFYIMTFLETLTMC 300				

Db	241	anwlaagfggpttlllgirgnanttgrilllvidekkmekislmtyimntflftlwgpr	3000
Oy	301	YLIVACIYMWVEFKRGVYVPGGFLTAAYVMMSFAOAGINPVCVCFPSNRELNRCSITLLYCRKS	3600
Db	301	ylvaciywvrfargpvpvgpfltaayvmmsfaagapnlpvcifpsnrelrcsttlllycrks	3600
Oy	361	RLPREPYCVI 370	
Db	361	rlprepycvi 370	
RESULT 4			
ID	AA02837	standard; Protein: 370 AA.	
XX	AA02837:		
XX	22-AUG-2000	(first entry)	
XX	Human: G protein coupled receptor hCHN3 protein SEQ ID NO:28.		
XX	Human: G protein-coupled receptor; GPCR; transmembrane receptor;		
KW	identification; agonist; screening; therapeutic; pharmaceutical;		
XX	mutant.		
OS	Homo sapiens.		
XX	MO200022131-A2.		
PD	20-APR-2000.		
XX	13-OCT-1999:	99WC-0524065.	
XX	13-OCT-1998:	98US-01704596.	
PR	12-NOV-1998:	98US-0108029.	
PR	20-NOV-1998:	98US-0109213.	
PR	27-NOV-1998:	98US-0110060.	
PR	16-FEB-1999:	99US-0120416.	
PR	26-FEB-1999:	99US-0121852.	
PR	12-MAR-1999:	99US-0123944.	
PR	12-MAR-1999:	99US-0123945.	
PR	12-MAR-1999:	99US-0123946.	
PR	12-MAR-1999:	99US-0123948.	
PR	12-MAR-1999:	99US-0123949.	
PR	12-MAR-1999:	99US-0123951.	
PR	28-MAY-1999:	99US-0136436.	
PR	28-MAY-1999:	99US-0136437.	
PR	28-MAY-1999:	99US-0136439.	
PR	28-MAY-1999:	99US-0137127.	
PR	28-MAY-1999:	99US-0137131.	
PR	28-MAY-1999:	99US-0137567.	
PR	30-JUN-1999:	99US-0141448.	
PR	27-AUG-1999:	99US-0151114.	
PR	03-SEP-1999:	99US-0152524.	
PR	29-SEP-1999:	99US-0156533.	
PR	29-SEP-1999:	99US-0156555.	
PR	29-SEP-1999:	99US-0156634.	
XX	(AREN-) ARENA PHARM INC.		
XX	Behan DP, Lehmann-Brunisma K, Chalmers DT, Chen R, Dang HT;		
PI	Gore M, Liss CW, Llin I, Lowltz K, White C;		
XX	WPI: 2000-317986/27.		
XX	N-PSDB: AAA46031.		
XX	Non-endogenous, human G protein-coupled receptors for screening		
PT	receptor, inverse or partial agonists useful as therapeutic agents		
XX	Example 1; Page 104-105; 187pp; English.		
XX	The present invention describes transmembrane receptors, preferably		

The present invention describes transmembrane receptors, preferably

XX A G-protein coupled 7 transmembrane receptor (AXOR-1).

DE Human: G-protein coupled seven transmembrane receptor; AXOR-1; infection;
 XX HIV-1; HIV-2; cancer; diabetes; obesity; anorexia; bulimia; asthma;
 KW Parkinson's disease; acute heart failure; hypotension; hypertension;
 KW urinary retention; osteoporosis; angina pectoris; myocardial infarction;
 KW stroke; ulcer; asthma; allergy; benign prostatic hypertrophy; migraine;
 KW vomiting; psychotic disorder; neurological disorder; dyskinesia.

XX Homo sapiens.

OS WO955734-A1.

PN 04-NOV-1999.

XX 20-APR-1999; 99WO-US08605.

PF 24-APR-1998; 98US-0082981.

PR 17-JUN-1998; 98US-0089639.

PR 16-FEB-1999; 99US-0251373.

XX (SMIK) SMITHKLINE BEECHAM CORP.

XX Bergsma D, Elshourbagy N, Shabon U;

PI WPI; 2000-116269/10.

DR N-PSDB; AA245608.

XX Novel G-protein coupled transmembrane receptor for use in the treatment
 PT and diagnosis of diseases such as diabetes and Parkinson's disease -
 PS Claim 1; Page 26; 40pp; English.

XX The present sequence represents a human G-protein coupled seven
 CC transmembrane receptor designated AXOR-1. The AXOR-1 polypeptide is
 CC used for diagnosing disease. It is also used for identifying agonists
 CC and antagonists. The AXOR-1 polynucleotide, polypeptide, agonists and
 CC antagonists can be used to treat conditions such as bacterial, fungal,
 CC viral infections, particularly HIV-1 or 2, cancers, diabetes, obesity,
 CC anorexia, bulimia, asthma, Parkinson's disease, acute heart failure,
 CC hypotension, hypertension, urinary retention, osteoporosis, angina
 CC pectoris, myocardial infarction, stroke, ulcers, asthma, allergies,
 CC benign prostatic hypertrophy, migraine, vomiting, psychotic,
 CC neurological disorders and dyskinesias. The AXOR-1 polypeptide can also
 CC be used as an immunogen to produce immunospecific antibodies and to
 CC produce an immunological response.

XX Sequence 370 AA;

SO

Query Match 100.0%; Score 1963; DB 21; Length 370;
 Best Local Similarity 100.0%; Pred. No. 2e-208;
 Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MANTSHADNLTQMSPLTAFKLTSLGFIIGSVVGNLISLLVKKTLRAAYFEL 60
 DB 1 manyshaadnlqnlspitafkltslgfiigsvvgnllsllyvkktlhrayyfl 60

QY 61 DDCSDILRSACIPFPVNSKNSSTWYGLTGVIAFLGVLSCEFHAFMFCISVTRY 120
 DB 61 dlccsdilrsacipfivnskngstwyglctkvialflgvsfhaafmfcisvtry 120

QY 121 LAIHHFFYKRLTFWTCIAVIGWMTLSVMAAPPVLDVGTYSFIREDDCTQHRSEF 180
 DB 121 laiahhrfytcrftfcclavlgmwltsvamalpvpvldvgtysfiredctqhrsef 180

QY 181 ANDSLGFMILLALILATOLVYIKLIFVHDHRRKKPVQFVAASQNTFFGPGASGOAA 240
 DB 181 andslgfmllalilatlqlyvlyklifvhdrrmkpvgfvaasqntffgpgasgaa 240

QY 241 ANNLAGEGRPTPTLLGIQNANTGRRRLVLDERMEKRISRMFYIMFLETLTNGP 300
 DB 241 annlaggrptptllgignantgrrrlvldermekrisrmfymfletltngp 300

DB 241 annlaggrptptllgignantgrrrlvldermekrisrmfymfletltngp 300

QY 301 YLVACYRWVFARGPVYFGGFTAAVWMSFAOGINPEFCISNRELRCEFTLLYCKRS 360
 DB 301 ylvacyrwvfargpvyvggftaavwmsfagaglnpfcilsnrelrcfstcllyckrs 360

QY 361 RLPREPYCVI 370
 DB 361 rlpncpycvl 370

RESULT 7
 AAB73558 standard; Protein: 370 AA.

ID AAB73558; AAB73558;

AC 07-AUG-2001 (first entry)

XX Human GP27-like G protein-coupled receptor HE8N124.

DE HE8N124: GP27-like G protein-coupled receptor; 7TM receptor;
 KW infection; viral; bacterial; fungal; protozoan; HIV-1;
 KW HIV-2; pain; cancer; diabetes; obesity; anorexia; bulimia;
 KW osteoporosis; asthma; allergy; urinary retention;
 KW acute heart failure; hypotension; hypertension; angina pectoris;
 KW myocardial infarction; stroke; ulcer; migraine; vomiting;
 KW psychotic disorder; neurological disorder; anxiety; schizophrenia;
 KW manic depression; bipolar disorder; depression; delirium; dementia;
 KW severe mental retardation; dyskinesia; Parkinson's disease;
 KW Huntington's disease; Gilles de la Tourette's syndrome; gene therapy;
 KW vaccine; drug screening; signal transduction.

XX Homo sapiens.

OS WO200132865-A1.

XX 10-MAY-2001.

PD 26-OCT-2000; 2000MO-BE10565.

PF 03-NOV-1999; 99EP-0121785.

PR (MERE) MERCK PATENT GMBH.

PA Kluxen F;

PI WPI; 2001-343484/36.

DR N-PSDB; AAH23853.

XX Novel GP27-like polypeptide, HE8N124, useful for treating diseases
 PT involving microbial infections, cancers, obesity, asthma, diabetes,
 PT hypotension, osteoporosis, myocardial infarction, Parkinson's disease
 PT Claim 3; Page 42; 45pp; English.

XX The invention relates to the human GP27-like G protein-coupled receptor
 CC HE8N124 (AAB73558), to cDNA encoding HE8N124 (AAH23853), and to HE8N124
 CC fragments and variants. Like all G protein-coupled receptors, HE8N124
 CC has 7 putative transmembrane domains and is involved in signal
 CC transduction. HE8N124 was found to be expressed in brain, heart atria,
 CC spleen, lung, placenta, bladder and testis. The invention also relates
 CC to recombinant expression of HE8N124, and to an HE8N124-specific
 CC antibody. HE8N124 proteins and nucleotides may be used to treat a wide
 CC variety of disorders including bacterial, fungal, protozoal and viral
 CC infections, particularly HIV-1 or HIV-2 infections; pain; cancers; benign
 CC prostatic hypertrophy; diabetes; obesity; anorexia; bulimia;
 CC osteoporosis; asthma; allergies; urinary retention; acute heart failure;
 CC hypotension; hypertension; angina pectoris; myocardial infarction;
 CC stroke; migraine; ulcers; vomiting; psychotic and neurological disorders
 CC such as anxiety, schizophrenia, manic depression, depression, delirium,

	CC	dementia's and severe mental retardation, and dyskinesias such as
	CC	Parkinson's disease, Huntington's disease or Gilles de la Tourette's
	CC	syndrome. HEBN124 proteins and nucleotides are useful as vaccines, and
	CC	HEBN124 proteins, nucleotides and antibodies may be used in screening
	CC	compounds for their ability to modulate HEBN124 activity or expression.
	CC	They are also useful for diagnosing or determining susceptibility of an
	CC	individual to a disease via the detection of abnormal levels of protein
	CC	or mRNA, or via the detection of mutations in the corresponding gene.
	CC	HEBN124 proteins are also useful for inducing an immunological response
	CC	in a mammal against the above diseases, for antibody production, and to
	CC	identify membrane bound or soluble receptors for HEBN124. HEBN124
	CC	nucleotides are also useful as diagnostic reagents and in chromosome
	CC	localisation and tissue expression studies. HEBN124-specific antibodies
	CC	are useful for purifying the HEBN124 protein or fragments thereof, and
	CC	are also useful for treating conditions associated with the expression of
	CC	the HEBN124 protein. The present sequence represents human HEBN124.
	CC	
	CC	
	xx	
SQ	Sequence	370 AA;
	Query Match	100.0%; Score 1963; DB 22; Length 370;
	Best Local Similarity	100.0%; Pred. No. 2e-208;
	Matches 370; Conservative	0; Mismatches 0; Indels 0; Gaps 0
OY	1	MANYSHADNTIQNISPLAFIKTISIGSLTICGVVGNILISTLLVKDKTLHAPYYELL 60
Db	1	manyshaadnllqnsplafikltslgflgsvvgnllisllvykdktlhnappyell 60
OY	61	DLCCSDIRSAICPFPEFVENSXKNGSWTGTGLTCRYIAFGVISCFTAEMLFCISVTRY 120
Db	61	dllccsdllrsalcifpfvfnsxknsgstwtgtglctckxiatfagviscftatmlfcisttry 120
OY	121	LAIAHHREYTKRLTFWTCLAVICMWTLSVANAAPPVLVDGYTSFIREDQCFFOHSFR 180
Db	121	laiahhrfytkrltfwclavicmwltlsavanaappvlvdgytysfiireeqdcffhsfr 180
OY	181	ANDSGFMILLALLATDYLVIKLIFPHDRKKMPVOCVAVASQWTHRGASQA 240
Db	181	andsigfmllalllatdylviklifphdrkkmpvovcvavasqwthrgasqa 240
OY	241	ANWLAFGFGPPTLTGLRONANTGRRLVLDEFKMKKRISRMYIMTFLELTLMGP 300
Db	241	anwlafgfgppptlltgirnanntggrrllvldefkmekrisrmymtffleltlmgp 300
OY	301	YLACYWRVFARGPVVGGELTAAMVMMSFAQAGINPFVCIFSNNELRCHSTLLYCCKS 360
Db	301	ylyacywrvfargpvvpvgfltaavmmsfaaglnpfvcifsnrelrcstlllycks 360
OY	361	RLPREPVCYT 370
Db	361	rllrepvcyt 370
RESULT	8	
AAE02497	ID	AAE02497 standard; Protein; 370 AA.
xx	xx	
AC	AAE02497;	
xx	xx	
DT	10-AUG-2001	(first entry)
xx	xx	
DE	Human CON202	G protein-coupled receptor protein.
xx	xx	
KW	Human; G protein-coupled receptor; GPCR; CON202 protein; schizophrenia;	
KW	neuroleptic; nootropic; neuroprotective; bipolar disease; schizophrenic;	
KW	neurological disorder; psychiatric disease; neurosis; anxiety; neuritis;	
KW	attention deficit hyperactivity disorder; neuropsychiatric; senile dementia;	
KW	affective disorder; neuropathy; Alzheimer's disease; Parkinson's disease;	
xx	depression; migraine; genetic screening; chromosome 7.	
OS	Homo sapiens.	
xx	xx	
Key	Location/Qualifiers	
TH		

FT	Domain	24..46	/label= Transmembrane_domain_(17M)
FT	Domain	47..56	/label= Intracellular_domain
FT	Domain	/note= "First IC loop"	
FT	Domain	57..77	/label= Transmembrane_domain_(27M)
FT	Domain	78..95	/label= Extracellular_domain
FT	Domain	/note= "First EC loop"	
FT	Domain	96..117	/label= Transmembrane_domain_(37M)
FT	Domain	118..134	/label= Intracellular_domain
FT	Domain	/note= "Second IC loop"	
FT	Domain	135..159	/label= Transmembrane_domain_(47M)
FT	Domain	160..183	/label= Extracellular_domain
FT	Domain	/note= "Second EC loop"	
FT	Domain	184..202	/label= Transmembrane_domain_(57M)
FT	Domain	203..285	/label= Intracellular_domain
FT	Domain	/note= "Thlrd IC loop"	
FT	Domain	286..308	/label= Transmembrane_domain_(67M)
FT	Domain	309..315	/label= Extracellular_domain
FT	Domain	/note= "Thlrd EC loop"	
FT	Domain	316..339	/label= Transmembrane_domain_(77M)
XX	WO200131014-A2.		
PN	03-MAY-2001.		
PD			
XX			
PE	27-OCT-2000; 2000WO-US29601.		
XX			
PR	27-OCT-1999; 99US-0427653.		
PR	27-OCT-1999; 99US-0427859.		
PR	27-OCT-1999; 99US-0428020.		
PR	27-OCT-1999; 99US-0428114.		
PR	28-OCT-1999; 99US-0428517.		
PR	28-OCT-1999; 99US-0429555.		
PR	28-OCT-1999; 99US-0429676.		
PR	28-OCT-1999; 99US-0429695.		
PR	03-DEC-1999; 99US-0454399.		
PR	12-JAN-2000; 2000US-0481794.		
XX			
PA	(PHNA) PHARMACIA & UPJOHN CO.		
PI	Vogeli G, Wood JS, Merchant K;		
XX			
DR	WPI; 2001-328653/34.		
XX	N-PSDB; AAD06506.		
PT			
PT	Seven transmembrane receptor polypeptides and polynucleotides, useful		
PT	for treating neurological or psychiatric disorders, e.g. schizophrenia,		
PT	as well as for identifying compounds useful for treating schizophrenia		
XX			
PS	Claim 1; Page 14-15; 215pp; English.		
XX			
CC	The invention relates to human G protein-coupled receptor (GPCR) and		
CC	their corresponding DNA molecules. GPCR is also referred as seven		
CC	transmembrane receptor. G protein-coupled receptor protein is useful for		
CC	treating neurological disorder, particularly schizophrenia. GPCR protein		
CC	is also useful for identifying compounds useful for treating		
CC	schizophrenia. These compounds are also useful for treating other		
CC	neurological and psychiatric diseases, e.g. depression, anxiety, bipolar		
CC	disease, affective disorders, attention deficit hyperactivity disorder/		
CC	attention deficit disorder, epilepsy, neuritis, neuroasthenia, neuropathy		
CC			

CC neurosis, Alzheimer's disease, Parkinson's disease, migraine and senile
CC dementia. The invention also provides genetic screening procedures that
CC entail analysing a person's genome with respect to GPCR. The vectors are
CC useful for the recombinant production of the GPCR's. The present sequence
CC is human CON202 G protein-coupled receptor (GPCR) protein.
XX
SQ Sequence 370 AA;

Query Match 100.0%; Score 1963; DB 22; Length 370;
Best Local Similarity 100.0%; Pred. No. 2e-208;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MANYSHADNIIQNLSPITAFKLTSGFTIGSVGNLIIITLVMDKTHRAPYFL 60
DB 1 manyshadniiqnlspitafkltsgftigsvgnlilistlvmdkthrapyyfl 60
QY 61 DDCSDILRSALCFPEFVNSVKNSTWYGTLCNKVIAFLGVLSCFPTAFELFCISVTRY 120
DB 61 ddcscdilsalcfpefvnsvknstwtgltcnkviaflgvlsctfatafclsvtry 120
QY 121 LAIAHREFTKLTFTWTCIAVICMWTLSVAMAPPVLDVGYVSFIREDOCTFQHSFR 180
DB 121 laiahreftkltftwtcclavicmwvlsvamafpvldvgtyvsfiredoctfghsfr 180
QY 181 ANDSGEMLLALILATOLVYIKLIFVDRKRMKPVQVYAASQWTHGPGASGOA 240
DB 181 andsgemllalilatlolvylklifvdrkrmkpvqvyaasqwthgpgasgaa 240
QY 241 ANWLAFGRGPPTLLIGIQONANTGRRLLVDEKMKKRISRMVYIMFLELTMP 300
DB 241 anwlagrgpptlligiqonantgrrllvldemkkrismvymflefletmp 300
QY 301 YLVACYWRVAFARQPVVGGFLTAVMMSFAQAGINPEVCIFSNRELRCFSTLLYCRKS 360
DB 301 ylvacywrvarfqpvvggfltavmmsfaqaglnpevcifsnrelrcfstllycrks 360
QY 361 RUPREYCVI 370
DB 361 rUpREyCVI 370

RESULT 9
AAM99955
ID AAM99955 standard; Protein; 379 AA.

XX AAM99955;

XX 04-JAN-2002 (first entry)

DE Human expressed polypeptide SEQ ID NO 79.

XX Human; nootropic; neuroprotective; cyostatic; dermatological; virucide;
KW immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary;
KW antiparkinsonian; antischizling; antiaiemac; antiathritic; cancer;
KW antirheumatic; hepatotropic; cerebroprotective; antiinflammatory;
KW antiallergic; antidiabetic; antilucer; anticonvulsant; antifungal;
KW antiparasitic; cardiant; immune disorder; cardiovascular disorder;
KW neurological disease; infection; nephrotropic; gene therapy; vaccine.

OS Homo sapiens.

XX WO20015387-A1.

XX 02-AUG-2001.

XX 17-JAN-2001; 2001WO-US01310.

XX 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.

PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 07-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0217487.
PR 11-JUL-2000; 2000US-0217496.
PR 14-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
PR 26-JUL-2000; 2000US-0220964.
PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226868.
PR 22-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227009.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229509.
PR 05-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231245.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235836.
PR 27-SEP-2000; 2000US-0235837.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.

13-OCT-2000; 2000US-0239937.
 PR 20-OCT-2000; 2000US-0240960.
 PR 20-OCT-2000; 2000US-0241221.
 PR 20-OCT-2000; 2000US-0241785.
 PR 20-OCT-2000; 2000US-0241786.
 PR 20-OCT-2000; 2000US-0241787.
 PR 20-OCT-2000; 2000US-0241808.
 PR 20-OCT-2000; 2000US-0241809.
 PR 20-OCT-2000; 2000US-0241826.
 PR 01-NOV-2000; 2000US-0244617.
 PR 08-NOV-2000; 2000US-0246474.
 PR 08-NOV-2000; 2000US-0246475.
 PR 08-NOV-2000; 2000US-0246476.
 PR 08-NOV-2000; 2000US-0246477.
 PR 08-NOV-2000; 2000US-0246478.
 PR 08-NOV-2000; 2000US-0246523.
 PR 08-NOV-2000; 2000US-0246524.
 PR 08-NOV-2000; 2000US-0246525.
 PR 08-NOV-2000; 2000US-0246526.
 PR 08-NOV-2000; 2000US-0246527.
 PR 08-NOV-2000; 2000US-0246528.
 PR 08-NOV-2000; 2000US-0246532.
 PR 08-NOV-2000; 2000US-0246609.
 PR 08-NOV-2000; 2000US-0246610.
 PR 08-NOV-2000; 2000US-0246611.
 PR 17-NOV-2000; 2000US-0249207.
 PR 17-NOV-2000; 2000US-0249208.
 PR 17-NOV-2000; 2000US-0249209.
 PR 17-NOV-2000; 2000US-0249210.
 PR 17-NOV-2000; 2000US-0249211.
 PR 17-NOV-2000; 2000US-0249212.
 PR 17-NOV-2000; 2000US-0249213.
 PR 17-NOV-2000; 2000US-0249214.
 PR 17-NOV-2000; 2000US-0249215.
 PR 17-NOV-2000; 2000US-0249216.
 PR 17-NOV-2000; 2000US-0249217.
 PR 17-NOV-2000; 2000US-0249218.
 PR 17-NOV-2000; 2000US-0249244.
 PR 17-NOV-2000; 2000US-0249245.
 PR 17-NOV-2000; 2000US-0249246.
 PR 17-NOV-2000; 2000US-0249265.
 PR 17-NOV-2000; 2000US-0249269.
 PR 17-NOV-2000; 2000US-0249297.
 PR 17-NOV-2000; 2000US-0249299.
 PR 17-NOV-2000; 2000US-0249300.
 PR 01-DEC-2000; 2000US-0250160.
 PR 01-DEC-2000; 2000US-0250391.
 PR 05-DEC-2000; 2000US-0251030.
 PR 05-DEC-2000; 2000US-0251988.
 PR 05-DEC-2000; 2000US-0256719.
 PR 06-DEC-2000; 2000US-0251479.
 PR 08-DEC-2000; 2000US-0251856.
 PR 08-DEC-2000; 2000US-0251868.
 PR 08-DEC-2000; 2000US-0251869.
 PR 08-DEC-2000; 2000US-0251989.
 PR 08-DEC-2000; 2000US-0251990.
 PR 11-DEC-2000; 2000US-0254097.
 PR 05-JAN-2001; 2000US-0259678.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Rosen CA, Barash SC, Ruben SM;
 XX
 DR WPI: 2001-465573/50.
 DR N-PSDB; AAI99567.
 XX
 XX Isolated digestive system associated polypeptide for treating,
 PT preventing and/or proposing disorders related to the digestive system
 PT including digestive system cancers and also for testing and detection
 PT e.g. diagnosis -
 XX
 PS Claim 11; SEQ ID NO 79; 509bp + Sequence Listing; English.
 XX

CC The invention relates to novel genes (AAI99548-AAI99604) and proteins
 CC (AAI99596-AAI99984) useful for preventing, treating or ameliorating
 CC medical conditions e.g. by protein or gene therapy. The genes are
 CC isolated from a range of human tissues disclosed in the specification.
 CC The nucleic acids, proteins, antibodies and (ant)agonists are useful
 CC in the diagnosis, treatment and prevention of: (a) cancer; e.g. breast
 CC and ovarian cancer and other cancers of the adrenal gland, bone, bone
 CC marrow, breast, gastrointestinal tract, liver, lung, or urogenital;
 CC (b) immune disorders e.g. Addison's disease, allergies, autoimmune
 CC haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
 CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative
 CC colitis; (c) cardiovascular disorders such as myocardial ischaemia;
 CC (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and
 CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
 CC and parasitic infections.
 CC Note: The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published-pct-sequences.
 CC
 XX
 SQ Sequence 379 AA:
 Query Match 100.0%; Score 1963; DB 22; Length 379;
 Best Local Similarity 100.0%; Pred. No. 2,1e-208;
 Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 1. MANYSHADNITONLSPLTAFKLTSLGFLIGSVVGNLLISILVAKDKTLHAPYFLL 60
 |||||||
 10 manyshaadnllgnlsplafkltslgfligsvvgnllisilvkdktlhapyl 69
 QY 61 DCCSDILRSALCEPFVNSVKNKSTWYGTGLCKVIAFLGLVLSCHTAPMLFCISVTRY 120
 |||||||
 70 dccsdilrsalcfpfvnsvknkstwygtglckviaflglvlschtafmfcisvtry 129
 Db 121 LAIAHREFTKRLTFMTCLAVICMWTLSVAMFPPVLDVGTSTFIREHQCFQRHSR 180
 |||||||
 130 laiahrfytkrllftwclavicmwtlsvamfppvldvgtstfiredqcfqhrstr 189
 Db 181 ANDSLGFMLLAILATOLVYLKLFVHRRKMKPVQFAVASONMTPHGGASGOAA 240
 |||||||
 190 andslgfmllailatqlvylklffvhdrrkmkpvqfvaavsgnwtphggaagaa 249
 QY 241 ANMLAGFGGPPPTLLGIRONANTGRRRLVLDFEKMKRISRMFYIMTFELTLMGP 300
 |||||||
 250 anmlagfggppptllgirtqanantgrrllvldefekmkrisrmfymtftlmgp 309
 Db 301 YLVACTWRVFAKGPVYVGGELTAAVMSFRQAGINPVCIFSNRELRCRSTLLCRKS 360
 |||||||
 310 ylvacywrvfargpvvpgflltaavmsfraqaginpvcifsnrelrcrstllcrks 369
 QY 361 RLPREPYCVI 370
 |||||||
 370 rlprepvcvi 379
 Db
 RESULT 10
 AAB68873
 ID AAB68873 standard; Protein; 370 AA.
 AC
 XX AAB68873;
 XX
 DT 24-APR-2001 (first entry)
 XX
 DE Human RECAP polypeptide, SEQ ID NO: 3.
 XX
 XX Human; RECAP; receptors and associated proteins; cerebroprotective;
 KW neurotrophic; neuroprotective; anticonvulsant; antiparkinsonian; anti-HIV;
 KW antidiabetic; immunostimulant; immunomodulator; antiinflammatory;
 KW antihypertensive; immunosuppressive; nephrotoxic; antitumor; thyromimetic;
 KW cytostatic; antibacterial; virucide; fungicide; protozoacide;
 KW antidiabetic; hepatocytic; gene therapy; infection; cancer.
 KW
 XX Homo sapiens.
 OS

XX PN WO200107612-A2.
 XX XX
 XX PD 01-FEB-2001.
 XX XX
 XX PF 21-JUL-2000; 2000WO-US20035.
 XX XX
 XX PR 21-JUL-1999; 99US-0145232.
 XX PR 07-OCT-1999; 99US-0158578.
 XX PR 12-NOV-1999; 99US-0165192.
 XX XX
 XX PA (INCYTE) INCYTE GENOMICS INC.
 XX XX
 XX PI Au-Young J, Bandman O, Tang YT, Yue H, Azimzai Y, Burford N;
 XX PI Baughn MR, Lu DM, Hillman JL, Patterson C, Lal P;
 XX DR WPI: 2001-168554/17.
 XX DR N-PSDB; AAF58597.
 XX PT Novel receptors and associated proteins for diagnosis and treatment of
 PT neurological disorders, immunological disorders including autoimmune/
 PT inflammatory disorders and cell proliferative disorders such as cancer
 PT
 XX PS Claim 1; Page 96; 128pp; English.

CC The present sequence is a human RECAP (receptors and associated
 CC proteins) polypeptide. RECAP polynucleotides and polypeptides are useful
 CC in the diagnosis, treatment and prevention of neurological disorders
 CC such as stroke, Alzheimer's disease, Pick's disease, Huntington's
 CC disease, dementia, Parkinson's disease, Down's syndrome, amyotrophic
 CC lateral sclerosis, multiple sclerosis, bacterial and viral meningitis,
 CC CJD (Creutzfeldt-Jakob disease), GSS (Gerstmann-Strausler-Scheinker
 CC syndrome), immunological disorders, including autoimmune/inflammatory
 CC disorders such as AIDS, Digeorge's syndrome, severe combined
 CC immunodeficiency disease (SCID), Chediak-Higashi syndrome, Cushing's
 CC disease, Addison's disease, autoimmune thyroiditis, Crohn's disease,
 CC diabetes mellitus, Good pasture's syndrome, gout, Grave's diseases,
 CC Hashimoto's thyroiditis, Sjogren's syndrome, Werner's syndrome, viral,
 CC bacterial, fungal, parasitic, protozoal, and helminthic infections; and
 CC cell proliferation disorders such as arteriosclerosis, atherosclerosis,
 CC cirrhosis, hepatitis and cancer.

XX SO Sequence 370 AA:

Query Match 99.8%; Score 1959; DB 22; Length 370;
 Best Local Similarity 99.7%; Pred. No. 5.5e-208;
 Matches 369; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 MANYSHADNITQNTSPLTAFKLTSLGFTIGSVVGNLLISILLVKDKTLHAPYFELL 60
 DB 1 manyshadnltqntspltaflkltslgftigsvvgnllisilvvkdktlhrapyfll 60
 OY 61 DCCGDIIRSAICFPEVENSNGSWTGTCTCKYIAFLGVSCHTAFMCISTRY 120
 DB 61 dccgdilrsaicfpvsnsgswtgtctckyiaflgvschtafmciistrv 120
 OY 121 LAIAHREFTKRLTEWTCIAVICMWTLSVAMAFPPVLVGTSTFREDOCTFOHRSR 180
 DB 121 laiahreftkrltewtciavicmwtlsvamafppvlvgtstfre doctfohrrsr 180
 OY 181 ANDSGFMILLALILATOLVYIKLIEFVHRRKMKPVQFAVAVSQNMTFHBGASGQA 240
 DB 181 andsgfmillalilatlolvylkliefvhrmkpvoqfaavsqnmtf hbgasgqa 240
 OY 241 ANMAGFGGPPPTLLGIRONANTGRRRLVLDFFKKEKRSKRFYIMTFPLLMGP 300
 DB 241 anmagfggppptllgironantgrrrlvldffkkekrskrfymtfpl lmgp 300
 OY 301 YLVACYWRFARGPVVGGFLTAAMVMSFAQGINPFCIFSNRELRRCFSTLLYCRKS 360
 DB 301 ylvacywrfargpvvpgfltaamvmsfaoginpfvcifsnre lrrcfstlllycrks 360

OY 361 RLPREYCVI 370
 DB 361 rlpreycvi 370

RESULT 11
 AAY71300
 ID AAY71300; standard; Protein: 373 AA.

AC AAY71300;

DT 02-NOV-2000 (first entry)

DE Human orphan G protein-coupled receptor hARE-2.

KW Human; orphan G protein-coupled receptor; GPCR; hARE-2; drug screening;

KM transmembrane receptor; expressed sequence tag; EST; signal cascade.

OS Homo sapiens.

PN WO200031258-A2.

PD 02-JUN-2000.

PE 13-OCT-1999; 99WO-US23687.

PR 20-NOV-1998; 98US-0109213.

PR 16-FEB-1999; 99US-0120416.

PR 26-FEB-1999; 99US-0121852.

PR 12-MAR-1999; 99US-0123946.

PR 12-MAR-1999; 99US-0123949.

PR 28-MAY-1999; 99US-0136436.

PR 28-MAY-1999; 99US-0136437.

PR 28-MAY-1999; 99US-0136439.

PR 28-MAY-1999; 99US-0136567.

PR 28-MAY-1999; 99US-0137131.

PR 29-JUN-1999; 99US-0141448.

PR 29-SEP-1999; 99US-0156555.

PR 29-SEP-1999; 99US-0156633.

PR 29-SEP-1999; 99US-0156634.

PR 01-OCT-1999; 99US-0156653.

PR 01-OCT-1999; 99US-0157281.

PR 01-OCT-1999; 99US-0157282.

PR 01-OCT-1999; 99US-0157293.

PR 01-OCT-1999; 99US-0157294.

PR 12-OCT-1999; 99US-0416760.

PR 12-OCT-1999; 99US-0417044.

PA (AREN-) ARENA PHARM INC.

PI Chen R, Dang HT, Llaw CW, Lin I;

DR WPI: 2000-40068/34.

DR N-PSDB; AAD01127.

Novel human orphan G protein-coupled receptors and the encoding cDNAs
 for use in the identification of G protein-coupled receptor agonists -

Claim 38; Page 67-68; 102pp; English.

The present amino acid sequence is the hARE-2, an endogenous human
 orphan G protein-coupled receptor (GPCR), expressed in the left and
 right cerebellum. The hARE-2 cDNA was identified using ESTs (expressed
 sequence tag) A1090920 and 68530 as a probe.
 The orphan GPCR of the invention, like all GPCRs has seven transmembrane
 C-terminal. However, no endogenous ligands has yet been identified for
 the proteins of the invention. The orphan GPCRs may be used in the
 identification of their endogenous ligands, and to screen potential GPCR
 agonists and antagonists for use as pharmaceutical agents. The proteins

PR 12-MAR-1999; 99US-0123946.

Db 359 gtgagapaprepycvm 373

inverse agonists or partial agonists for use as pharmaceutical agents. AAAA6017 to AAAA6126 and AAB02825 to AAB02859 represent sequences used in

Query Match	65.6%;	Score 1288.5;	DB 21;	Length 373;
Best Local Similarity	62.7%;	Pred. No. 8.3e-134;		
Matches 235;	Conservative 56;	Mismatches 77;	Indels 7;	Gaps 4;

Db 300 spylvacgryvtvfkacavphrylatawmsfagaavnpvfcfllnklkcltrhapcw 359

Qy 357 CRKSLRPREPCVI 370
: |||||:

Db 360 tggaparepvcvm 373

RESULT 14
AAV97747
ID AAV97747 standard; Protein; 373 AA.
XX
AC AAV97747;
XX
DT 06-AUG-2001 (first entry)
XX
DE Human Monalisa protein sequence.
XX
KW Monalisa; human; G-protein coupled receptor; infection;1 HIV-1; HIV-2;
KW pain; cancer; diabetes; obesity; anorexia; bulimia; asthma; hypotension;
KW Parkinson's disease; acute heart failure; hypertension; osteoporosis;
KW urinary retention; angina pectoris; myocardial infarction; stroke; ulcer;
KW allergy; benign prostatic hypertrophy; migraine; psychotic disorder;
KW neurological disorder; anxiety; schizophrenia; manic depression;
KW delirium; dementia; severe mental retardation; dyskinesia; therapy;
KW Huntington's disorder; Gilles dela Tourette's syndrome.
XX
XX Homo sapiens.
OS
PN WO200132833-A2.
XX
PD 10-MAY-2001.
XX
PF 06-NOV-2000; 2000MO-US30541.
XX
PR 04-NOV-1999; 99US-0433840.
XX
PA (SMIK) SMITHKLINE BEECHAM CORP.
PA (SMIK) SMITHKLINE BEECHAM PLC.
XX
PI Zhu Y, Li X, Vawter L;
XX
DR MPI: 2001-335827/35.
DR N-PSDB; AAA91486.
XX
PT New Monalisa G-protein coupled receptor polypeptides and
PT polynucleotides, useful for treating certain diseases (e.g. infections,
PT pain or cancers), in diagnostic assays, or for identifying compounds
PT for therapy
XX
XX
XX
PS Claim 1; Page 27; 32pp; English.
XX
CC This sequence is the human Monalisa protein of the invention.. The
CC Monalisa protein is a member of the G-protein coupled receptor family.
CC The Monalisa polypeptide and polynucleotide are useful for treating
CC infections e.g. bacterial, fungal or viral infections particularly those
CC caused by HIV-1 or HIV-2. The Monalisa sequences are also useful for
CC treating pain, cancers, diabetes, obesity, anorexia, bulimia, asthma,
CC Parkinson's disease, acute heart failure, hypotension, hypertension,
CC urinary retention, osteoporosis, angina pectoris, myocardial infarction,
CC stroke, ulcers, allergies, benign prostatic hypertrophy, migraine,
CC vomiting, psychotic and neurological disorders (including anxiety,
CC schizophrenia, manic depression, delirium, dementia, and severe mental
CC retardation), dyskinesias, Huntington's disorder, and Gilles dela
CC Tourette's syndrome. The Monalisa polypeptide and polynucleotide are also
CC useful in diagnostic assays, as well as in identifying compounds
CC (e.g. agonists or antagonists) that are potentially useful in therapy.
XX
SQ Sequence 373 AA;

Query Match 65.4%; Score 1283.5; DB 22; Length 373;
Best Local Similarity 62.3%; Pred. No. 3e-133;
Matches 233; Conservative 56; Mismatches 80; Indels 5; Gaps 3

[illegible]

RESULT 15
AAM99953
ID AAM99953 standard; Protein; 378 AA

AC AAM99953;

DT 04-JAN-2002 (first entry)

DE Human expressed polypeptide SEQ ID NO 77

KW Human, ootrophic; neuroprotective; cytostatic; dermatological; virocidic
KW immunosuppressive; antiinflammatory; anti-HIV, antibacterial; vulnerary
KW antiparkinsonian; antischling; antianemic; antiarthritic; cancer;
KW antipneumatic; hepatotropic; cerebroprotective; antiinflammatory;
KW antiallergic; antidiabetic; antilucer; anticonvulsant; antifungal;
KW antiparastatic; cardiac; immune disorder; cardiovascular disorder
KW neurological disease; infection; nephrotropic; gene therapy; vaccine.

OS Homo sapiens.

PN W0200155387-A1..

PD 02-AUG-2001.

17-JAN-2001; 2001WO-US01310.

PR 31-JAN-2000; 2000US-0179065

PR 24-FEB-2000; 2000US-0184664

PR 16-MAR-2000; 2000US-0189874

PR 18-APR-2000; 2000US-0198123

PR 07-JUN-2000; 2000US-0209467

PR 30-JUN-2000; 2000US-0215135

PR 07-JUL-2000; 2000US-0216880
PR 11-JUL-2000; 2000US-0217487

PR 11-JUL-2000; 2000US-0217496

PR 26-JUL-2000; 2000US-0220963

PR	16-JUL-2000	2000US-02209661
PR	14-AUG-2000	2000US-02245180
PR	14-AUG-2000	2000US-02245181
PR	14-AUG-2000	2000US-02245213
PR	14-AUG-2000	2000US-02252114
PR	14-AUG-2000	2000US-02252666
PR	14-AUG-2000	2000US-02252677
PR	14-AUG-2000	2000US-02252679
PR	14-AUG-2000	2000US-02252681
PR	14-AUG-2000	2000US-02252682
PR	22-AUG-2000	2000US-02261862
PR	22-AUG-2000	2000US-02261868
PR	30-AUG-2000	2000US-02270091
PR	01-SEP-2000	2000US-02282924
PR	01-SEP-2000	2000US-02282927
PR	01-SEP-2000	2000US-02282937
PR	01-SEP-2000	2000US-02283443
PR	01-SEP-2000	2000US-02283444
PR	01-SEP-2000	2000US-02283577
PR	01-SEP-2000	2000US-02283585
PR	05-SEP-2000	2000US-02282559
PR	05-SEP-2000	2000US-02283505
PR	05-SEP-2000	2000US-02283549
PR	06-SEP-2000	2000US-02285131
PR	06-SEP-2000	2000US-02304377
PR	06-SEP-2000	2000US-02304378
PR	08-SEP-2000	2000US-02313243
PR	08-SEP-2000	2000US-02313243
PR	08-SEP-2000	2000US-02313243
PR	08-SEP-2000	2000US-02313244
PR	08-SEP-2000	2000US-02313413
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PR	08-SEP-2000	2000US-02314114
PR	08-SEP-2000	2000US-02330881
PR	08-SEP-2000	2000US-02330882
PR	08-SEP-2000	2000US-02330883
PR	12-SEP-2000	2000US-02331967
PR	14-SEP-2000	2000US-02333397
PR	14-SEP-2000	2000US-02333398
PR	14-SEP-2000	2000US-02333398
PR	14-SEP-2000	2000US-02333399
PR	14-SEP-2000	2000US-02333400
PR	14-SEP-2000	2000US-02334001
PR	14-SEP-2000	2000US-02334013
PR	14-SEP-2000	2000US-02330654
PR	14-SEP-2000	2000US-02330654
PR	14-SEP-2000	2000US-02330655
PR	21-SEP-2000	2000US-02342323
PR	21-SEP-2000	2000US-02342325
PR	21-SEP-2000	2000US-02342974
PR	25-SEP-2000	2000US-02343677
PR	25-SEP-2000	2000US-02343677
PR	25-SEP-2000	2000US-02343683
PR	25-SEP-2000	2000US-02343684
PR	27-SEP-2000	2000US-02358634
PR	27-SEP-2000	2000US-02358636
PR	29-SEP-2000	2000US-02353827
PR	29-SEP-2000	2000US-02353827
PR	29-SEP-2000	2000US-02353827
PR	29-SEP-2000	2000US-02353827
PR	29-SEP-2000	2000US-02353827
PR	29-SEP-2000	2000US-02353827
PR	29-SEP-2000	2000US-02353827
PR	02-OCT-2000	2000US-02368602
PR	02-OCT-2000	2000US-02370307
PR	02-OCT-2000	2000US-02370307
PR	02-OCT-2000	2000US-02370308
PR	02-OCT-2000	2000US-02370309
PR	02-OCT-2000	2000US-02370309
PR	13-OCT-2000	2000US-02393935
PR	13-OCT-2000	2000US-02393935
PR	13-OCT-2000	2000US-02393937
PR	13-OCT-2000	2000US-02393937
PR	20-OCT-2000	2000US-02411221
PR	20-OCT-2000	2000US-02411221
PR	20-OCT-2000	2000US-02411221
PR	20-OCT-2000	2000US-02411785
PR	20-OCT-2000	2000US-02417867
PR	20-OCT-2000	2000US-02417876
PR	20-OCT-2000	2000US-02417877
PR	20-OCT-2000	2000US-02418708
PR	20-OCT-2000	2000US-02418708
PR	20-OCT-2000	2000US-02418709
PR	20-OCT-2000	2000US-02418709
PR	01-NOV-2000	2000US-02446174
PR	01-NOV-2000	2000US-02446174
PR	08-NOV-2000	2000US-02446475
PR	08-NOV-2000	2000US-02446475

PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
XX
PA (HOMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Barash SC, Ruben SM;
XX
DR WPI: 2001-465573/50.
XX N-PSDB:AAI99565.
XX
PT Isolated digestive system associated polypeptide for treating,
PT preventing and/or prognosing disorders related to the digestive system
PT including digestive system cancers and also for testing and detection
PT e.g. diagnosis -
XX
PS Claim 11; SEQ ID NO 77; 509pp + Sequence Listing; English.
XX
CC The invention relates to novel genes (AAI99548-AAI99604) and proteins
CC (AAM99936-AAM99984) useful for preventing, treating or ameliorating
CC medical conditions e.g. by protein or gene therapy. The genes are
CC isolated from a range of human tissues disclosed in the specification.
CC The nucleic acids, proteins, antibodies and (ant)agonists are useful
CC in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast
CC and ovarian cancer and other cancers of the adrenal gland, bone, bone
CC marrow, breast, gastrointestinal tract, liver, lung, or urogenital;
CC (b) immune disorders e.g. Addison's disease, allergies, autoimmune
CC haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative
CC colitis; (c) cardiovascular disorders such as myocardial ischaemias;

CC (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and
CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
CC and parasitic infections.
CC Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from Wipo at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 378 AA;

Query Match 65.4%; Score 1283.5; DB 22; Length 378;
Best Local Similarity 62.3%; Pred. No. 3e-133;
Matches 233; Conservative 56; Mismatches 80; Indels 5; Gaps 3;

QY 1 MANYSHADNIONLSP--LTAFLKLSLGIIGSVYGNLLISLLWKDTRLRAPYF 58
Db manttgeeevsagalsppasaykllvlglmcsnagallslvlkeralkkpyf 65
QY 59 LLDLCCSDILRSALCPFFVNSVKNSTWYTGILTCVIAFLGVLSCPHTAFLCISVT 118
Db lldlcladgirsavcfpfvlasvthgsswtfsalscklvaflmavllfcfhaflfcisvt 125
QY 119 RYLAIAHREYTRKLPFTGLAVICWVWTLISVAMAFPPVLDVGYTSFTREDOCTFHRS 178
Db rymalahrtyakrmtlwtcaavycmawtlsvamafppvldvgytklireedqclfenty 185
QY 179 FRANDSLGFMLLALILATOLVYLKLFVHDKKKPVQFVAVSQNTFHPGASQ 238
Db fkancltglmmlavlmachavgyklllfeytrkknkqymvpaigntvfhgpgatg 245
QY 239 AANWLAGFGRGPPPTLLIRONANTTGRRLILVDEFKMKRISRMFYIMFLPLTW 298
Db aaanwlagfgrgmpplllgtrgghaas--rllgmdevkxgkqlymfaatlillw 304
QY 299 GPYLVCYWRVFARGPVPGGLFLAAYWMSFAQGINPFCIFENRRLRCFST--TLTY 356
Db 305 spyivacywrvfakacaphrlylatavmsfagaavpivcflinkdkclrlhapcw 364
QY 357 CRKSRLPREPCVY 370
Db 365 tggapaprepcvm 378

Search completed: July 19, 2002, 14:39:18
Job time: 354 sec

